

SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd.

<120> TRANSFORMED CELL WITH ENHANCED SENSITIVITY TO ANTIFUNGAL COMPOUN
D AND USE THEREOF

<130>

<160> 90

<210> 1

<211> 1315

<212> PRT

<213> Botryotinia fuckeliana

<400> 1

Met Glu Asp Ser Thr Ile Ala His Thr Thr Ala Ile Leu Gln Thr Leu

1 5 10 15

Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys

20 25 30

Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu

35 40 45

Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg

50 55 60

Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu

65 70 75 80

Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg

85	90	95
Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu		
100	105	110
Ala Ala Arg Glu Ala Pro Thr Gly Gly Glu Arg Pro Pro Lys Phe Thr		
115	120	125
Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His		
130	135	140
Gln Ser Lys Gln Leu Asp Ser Gln Lys Ser Glu Leu Ala Gly Val His		
145	150	155
Ala Gln Leu Phe Glu Gln Lys Gln Arg Gln Glu Gln Ala Leu Asn Val		
165	170	175
Leu Glu Val Glu Arg Val Ala Ala Leu Glu Arg Glu Leu Lys Lys His		
180	185	190
Gln Gln Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu		
195	200	205
Ile Val Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Gln Ile		
210	215	220
His Ser Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Val Ile		
225	230	235
Asn Thr Met Met Asp Gln Leu Gln Ile Phe Ser Ser Glu Val Ser Arg		
245	250	255
Val Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Lys		
260	265	270
Ile Ser Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn		
275	280	285
Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val		

290	295	300	
Thr Thr Ala Val	Ala His Gly Asp Leu Thr	Gln Lys Ile Glu Arg Pro	
305	310	315	320
Ala Gln Gly Glu Ile	Leu Gln Leu Gln Gln Thr	Ile Asn Thr Met Val	
	325	330	335
Asp Gln Leu Arg Thr	Phe Ala Ala Glu Val Thr	Arg Val Ala Arg Asp	
	340	345	350
Val Gly Thr Glu Gly	Ile Leu Gly Gly Gln Ala Glu	Ile Glu Gly Val	
	355	360	365
Gln Gly Met Trp Asn	Thr Leu Ile Val Asn Val	Asn Ala Met Ala Asn	
	370	375	380
Asn Leu Thr Thr Gln	Val Arg Asp Ile Ala Ile	Val Thr Thr Ala Val	
385	390	395	400
Ala Lys Gly Asp Leu	Thr Gln Lys Val Gln Ala	Glu Cys Lys Gly Glu	
	405	410	415
Ile Lys Gln Leu Lys	Glu Thr Ile Asn Ser Met	Val Asp Gln Leu Gln	
	420	425	430
Gln Phe Ala Arg Glu	Val Thr Lys Ile Ala Arg	Glu Val Gly Thr Glu	
	435	440	445
Gly Arg Leu Gly Gly	Gln Ala Thr Val His Asp	Val Glu Gly Thr Trp	
	450	455	460
Arg Asp Leu Thr Glu	Asn Val Asn Gly Met Ala	Met Asn Leu Thr Thr	
465	470	475	480
Gln Val Arg Glu Ile	Ala Lys Val Thr Thr	Ala Val Ala Arg Gly Asp	
	485	490	495
Leu Thr Lys Lys Ile	Glu Val Glu Val Gln Gly	Glu Ile Ala Ser Leu	

500	505	510
Lys Asp Thr Ile Asn Thr Met Val Asp Arg Leu Ser Thr Phe Ala Phe		
515	520	525
Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly		
530	535	540
Gly Gln Ala Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr		
545	550	555
Glu Asn Val Asn Thr Met Ala Arg Asn Leu Thr Thr Gln Val Arg Gly		
565	570	575
Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Gln Lys		
580	585	590
Ile Glu Val Ala Ala Ala Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile		
595	600	605
Asn Asn Met Val Asp Arg Leu Ser Ile Phe Ser Asn Glu Val Gln Arg		
610	615	620
Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln Ala Asp		
625	630	635
Val Ala Gly Ile Gly Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn		
645	650	655
Thr Met Ala Asn Asn Leu Thr Thr Gln Val Arg Ala Phe Gly Asp Ile		
660	665	670
Thr Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Ile Thr Val Glu		
675	680	685
Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val		
690	695	700
Tyr Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Leu Ala Arg Glu Ala		

705	710	715	720
Ala Glu Phe	Ala Asn Arg Thr Lys Ser Glu Phe	Leu Ala Asn Met Ser	
725	730	735	
His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu			
740	745	750	
Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile			
755	760	765	
Val His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu			
770	775	780	
Asp Leu Ser Lys Ile Glu Ala Asn Arg Met Ile Met Glu Glu Ile Pro			
785	790	795	800
Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val			
805	810	815	
Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser			
820	825	830	
Val Pro Asp His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Val Ile			
835	840	845	
Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val			
850	855	860	
Ser Leu Thr Ile Gln Lys Ala Glu Gln Asp His Cys Ala Pro Asn Glu			
865	870	875	880
Tyr Ala Val Glu Phe Cys Val Ser Asp Thr Gly Ile Gly Ile Gln Ala			
885	890	895	
Asp Lys Leu Asn Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser			
900	905	910	
Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys			

915	920	925	
Arg Leu Val Asn Leu Met Arg Gly Asp Val Trp Val Lys Ser Gln Tyr			
930	935	940	
Gly Lys Gly Ser Ser Phe Tyr Phe Thr Cys Thr Val Arg Leu Ala Thr			
945	950	955	960
Ser Asp Ile Ser Phe Ile Gln Lys Gln Leu Lys Pro Tyr Gln Gly His			
965	970	975	
Asn Val Leu Phe Ile Asp Lys Gly Gln Thr Gly His Gly Lys Glu Ile			
980	985	990	
Ile Thr Met Leu Thr Gln Leu Gly Leu Val Pro Val Val Val Asp Ser			
995	1000	1005	
Glu Gln His Thr Ile Leu Leu Gly Asn Gly Arg Thr Lys Glu Lys Ile			
1010	1015	1020	
Ala Ser Thr Tyr Asp Val Ile Val Val Asp Ser Ile Glu Ser Ala Arg			
1025	1030	1035	1040
Lys Leu Arg Ser Ile Asp Glu Phe Lys Tyr Ile Pro Ile Val Leu Leu			
1045	1050	1055	
Ala Pro Val Ile His Val Ser Leu Lys Ser Ala Leu Asp Leu Gly Ile			
1060	1065	1070	
Thr Ser Tyr Met Thr Thr Pro Cys Leu Thr Ile Asp Leu Gly Asn Gly			
1075	1080	1085	
Met Ile Pro Ala Leu Glu Asn Arg Ala Ala Pro Ser Leu Ala Asp Asn			
1090	1095	1100	
Thr Lys Ser Phe Asp Ile Leu Leu Ala Glu Asp Asn Ile Val Asn Gln			
1105	1110	1115	1120
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val			

1125	1130	1135	
Val Gly Asn Gly Gln Glu Ala Leu Asp Ala Ile Lys Glu Lys Arg Tyr			
1140	1145	1150	
Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu			
1155	1160	1165	
Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg			
1170	1175	1180	
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu			
1185	1190	1195	1200
Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys			
1205	1210	1215	
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly			
1220	1225	1230	
Ala Leu Leu Glu Lys Gly Arg Glu Val Arg Gln Ser Ala Asn Glu Glu			
1235	1240	1245	
Ser Pro Asn Ser Gln Asn Gly Pro Arg Gly Thr Gln His Pro Ala Ser			
1250	1255	1260	
Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr			
1265	1270	1275	1280
Thr Thr Thr Gly Pro Ile Asn His Gly Ser Ala Glu Ser Pro Ser Leu			
1285	1290	1295	
Val Thr Ala Asp Ala Glu Asp Pro Leu Ala Arg Leu Leu Met Arg Ala			
1300	1305	1310	
His Ser Ser			
1315			

<210> 2

<211> 3948

<212> DNA

<213> Botryotinia fuckeliana

<220>

<221> CDS

<222> (1).. (3948)

<400> 2

atg gag gat tct aca ata gct cat act act gcg atc ctg caa act ctc 48

Met Glu Asp Ser Thr Ile Ala His Thr Thr Ala Ile Leu Gln Thr Leu

1 5 10 15

gca tta tcg agc atc gat ctt cca ctg acg aat gtt tac ggc aac aag 96

Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys

20 25 30

ggg att agg tta cca ggt gca gat acg gca gag aag ctt gcc ctc gaa 144

Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu

35 40 45

cga gaa ctt gcg gcc ttg gta tcc aga gtc caa aga tta gaa gca agg 192

Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg

50 55 60

gcg atc aca gtc aat aat caa acc ctg ccc gat acg ccg aat gaa tta	240
Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu	
65 70 75 80	
gga gcg cca tct gct ttc gca gat gta ctc act ggt gcc cca tcc cga	288
Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg	
85 90 95	
gcc tca aag agt act aca tcc cga caa cag ctc gta aat tcg ttg ctt	336
Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu	
100 105 110	
gcc gcc aga gaa gcg ccc acc ggc ggt gaa aga cct cct aaa ttt acg	384
Ala Ala Arg Glu Ala Pro Thr Gly Gly Glu Arg Pro Pro Lys Phe Thr	
115 120 125	
aaa tta agt gac gag gaa ctc gaa gca ctc cgc gaa cat gtc gac cat	432
Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His	
130 135 140	
caa tcg aaa caa ctc gat agt caa aaa tct gag ctg gcc ggt gta cat	480
Gln Ser Lys Gln Leu Asp Ser Gln Lys Ser Glu Leu Ala Gly Val His	
145 150 155 160	
gct caa ctg ttt gag cag aag cag aga caa gaa caa gca ctc aac gtt	528

Ala Gln Leu Phe Glu Gln Lys Gln Arg Gln Glu Gln Ala Leu Asn Val

165

170

175

ctt gaa gtc gaa cgc gta gca gct ctc gaa aga gaa ctg aag aag cat 576

Leu Glu Val Glu Arg Val Ala Ala Leu Glu Arg Glu Leu Lys Lys His

180

185

190

caa caa gcc aac gag gct ttc caa aaa gct cta cgg gaa ata gga gag 624

Gln Gln Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu

195

200

205

att gtc aca gct gta gct agg ggt gat ctc agt aag aag gta caa atc 672

Ile Val Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Gln Ile

210

215

220

cac tcc gtg gag atg gac cct gag att aca act ttc aag cgt gtt att 720

His Ser Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Val Ile

225

230

235

240

aat act atg atg gat caa ctt cag ata ttc tct agt gag gtt tct cgt 768

Asn Thr Met Met Asp Gln Leu Gln Ile Phe Ser Ser Glu Val Ser Arg

245

250

255

gta gct aga gag gtc ggc aca gaa ggt att ctc ggt gga caa gcc aag 816

Val Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Lys

260

265

270

att tct ggt gtt gat ggt aca tgg aag gag ttg act gac aat gtc aac	864
Ile Ser Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn	
275 280 285	
ggt atg gca caa aat ctc acc gat caa gtc cga gaa att gct tcc gtc	912
Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val	
290 295 300	
act act gct gta gct cat gga gat ctc aca caa aag att gag aga cca	960
Thr Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Arg Pro	
305 310 315 320	
gcc cag ggt gag ata ctc caa ctg caa caa act atc aat acc atg gtg	1008
Ala Gln Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val	
325 330 335	
gat caa ttg aga acg ttc gcc gcc gag gtc acc cgc gta gca aga gat	1056
Asp Gln Leu Arg Thr Phe Ala Ala Glu Val Thr Arg Val Ala Arg Asp	
340 345 350	
gta gga act gaa ggt att ctt ggg ggt caa gca gaa atc gaa ggc gtc	1104
Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Glu Ile Glu Gly Val	
355 360 365	
cag ggc atg tgg aac aca ttg ata gtg aac gtc aac gct atg gcc aat	1152

Gln Gly Met Trp Asn Thr Leu Ile Val Asn Val Asn Ala Met Ala Asn	
370	375 380
aac ctc acc aca caa gtg cgc gat ata gcc att gtc aca aca gct gtc	1200
Asn Leu Thr Thr Gln Val Arg Asp Ile Ala Ile Val Thr Thr Ala Val	
385	390 395 400
gca aag gga gac ctg act caa aag gtc caa gca gaa tgt aag ggt gaa	1248
Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Lys Gly Glu	
405	410 415
atc aag cag ttg aag gag act ata aat tcc atg gtg gac caa tta caa	1296
Ile Lys Gln Leu Lys Glu Thr Ile Asn Ser Met Val Asp Gln Leu Gln	
420	425 430
caa ttt gcg cga gaa gtc acg aag att gct agg gag gtc ggt acc gaa	1344
Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu	
435	440 445
ggt aga ctg ggt gga caa gca aca gtg cat gat gtt gaa ggc act tgg	1392
Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly Thr Trp	
450	455 460
aga gac ctc acc gaa aat gtg aat ggt atg gcc atg aat ctt acg aca	1440
Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr	
465	470 475 480

caa gta cga gag att gca aag gtt acc acc gct gtc gcc aga gga gat	1488
Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Arg Gly Asp	
485 490 495	
ttg acc aag aag att gaa gtc gag gtt cag gga gaa atc gct tcg ctg	1536
Leu Thr Lys Lys Ile Glu Val Glu Val Gln Gly Glu Ile Ala Ser Leu	
500 505 510	
aaa gat acc atc aac acc atg gtg gac aga ctt agt aca ttc gct ttt	1584
Lys Asp Thr Ile Asn Thr Met Val Asp Arg Leu Ser Thr Phe Ala Phe	
515 520 525	
gag gtt agc aaa gtc gcc agg gag gtc gga act gat ggg act ctt ggt	1632
Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly	
530 535 540	
gga caa gcg caa gtt gat aac gtc gaa gga aag tgg aaa gac ctc act	1680
Gly Gln Ala Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr	
545 550 555 560	
gaa aat gtg aac acc atg gcc aga aac ttg act act caa gta cga ggt	1728
Glu Asn Val Asn Thr Met Ala Arg Asn Leu Thr Thr Gln Val Arg Gly	
565 570 575	
atc tcg act gtt aca caa gct att gcc aat gga gac atg agt cag aag	1776

Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Gln Lys

580

585

590

att gag gtt gct gct gcg ggt gaa ata ctc ata cta aag gaa acc ata 1824

Ile Glu Val Ala Ala Ala Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile

595

600

605

aat aac atg gta gac aga ttg agt atc ttc tcc aac gaa gtg caa aga 1872

Asn Asn Met Val Asp Arg Leu Ser Ile Phe Ser Asn Glu Val Gln Arg

610

615

620

gtc gcc aaa gat gtg ggt gtg gat ggt aag atg ggt ggc caa gct gac 1920

Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln Ala Asp

625

630

635

640

gtt gct ggg att ggc ggc cgt tgg aaa gag atc aca acg gat gtc aat 1968

Val Ala Gly Ile Gly Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn

645

650

655

acc atg gct aac aac ttg aca acc caa gtg cgc gcc ttt ggt gat ata 2016

Thr Met Ala Asn Asn Leu Thr Thr Gln Val Arg Ala Phe Gly Asp Ile

660

665

670

act aac gcc gca acc gat ggc gac ttc aca aaa ttg atc act gtc gag 2064

Thr Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Ile Thr Val Glu

675

680

685

gca tct gga gag atg gat gag ctg aag cga aag atc aac cag atg gtg	2112
Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val	
690 695 700	
tac aat ctg agg gac agt att caa aga aac acc ttg gct agg gag gct	2160
Tyr Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Leu Ala Arg Glu Ala	
705 710 715 720	
gcc gaa ttc gcc aat agg acg aag tct gaa ttc ttg gct aac atg tct	2208
Ala Glu Phe Ala Asn Arg Thr Lys Ser Glu Phe Leu Ala Asn Met Ser	
725 730 735	
cac gag att cga aca cct atg aac ggt atc att ggt atg act cag ttg	2256
His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu	
740 745 750	
aca ctc gac acc gat ctt act caa tat caa cga gaa atg ctc aac att	2304
Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile	
755 760 765	
gtt cac aac ttg gcc aac agt tta ttg acc atc att gat gat att ctc	2352
Val His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu	
770 775 780	
gat tta tca aag atc gaa gca aac cgt atg atc atg gag gag att cca	2400

gat aag ctc aat ttg att ttc gac act ttc caa caa gct gac gga tct	2736
Asp Lys Leu Asn Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser	
900 905 910	
atg acg agg aaa ttc gga ggt act ggt cta ggt cta tca att tcg aag	2784
Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys	
915 920 925	
aga ctt gta aac ctc atg cgt gga gat gtt tgg gtt aag agt cag tac	2832
Arg Leu Val Asn Leu Met Arg Gly Asp Val Trp Val Lys Ser Gln Tyr	
930 935 940	
gga aaa ggc agt tca ttc tac ttc acg tgt acc gtc cgc ctc gca acc	2880
Gly Lys Gly Ser Ser Phe Tyr Phe Thr Cys Thr Val Arg Leu Ala Thr	
945 950 955 960	
tca gat atc agt ttc att cag aaa caa ctc aag cca tat caa ggt cac	2928
Ser Asp Ile Ser Phe Ile Gln Lys Gln Leu Lys Pro Tyr Gln Gly His	
965 970 975	
aat gtt ttg ttt atc gac aaa gga cag act ggc cat ggc aaa gaa ata	2976
Asn Val Leu Phe Ile Asp Lys Gly Gln Thr Gly His Gly Lys Glu Ile	
980 985 990	
atc act atg ctt aca caa ctt ggt ttg gta ccc gtt gtt gtt gac tct	3024

Ile Thr Met Leu Thr Gln Leu Gly Leu Val Pro Val Val Val Asp Ser

995

1000

1005

gag cag cac act att ctt ctc ggc aat gga aga acc aag gag aag att 3072

Glu Gln His Thr Ile Leu Leu Gly Asn Gly Arg Thr Lys Glu Lys Ile

1010

1015

1020

gct tca act tat gac gtg att gtt gtg gac tca att gag tcc gct cga 3120

Ala Ser Thr Tyr Asp Val Ile Val Val Asp Ser Ile Glu Ser Ala Arg

1025

1030

1035

1040

aaa ctg cga tca atc gat gag ttc aag tat att cca att gtt ctc tta 3168

Lys Leu Arg Ser Ile Asp Glu Phe Lys Tyr Ile Pro Ile Val Leu Leu

1045

1050

1055

gct ccc gtt att cat gtc agc tta aag tct gct ttg gat ctt ggt atc 3216

Ala Pro Val Ile His Val Ser Leu Lys Ser Ala Leu Asp Leu Gly Ile

1060

1065

1070

act tct tac atg acc act cca tgt tta acg atc gat ctt ggc aat ggt 3264

Thr Ser Tyr Met Thr Thr Pro Cys Leu Thr Ile Asp Leu Gly Asn Gly

1075

1080

1085

atg att cct gct ttg gag aat cga gct gca ccc tca ttg gcg gac aac 3312

Met Ile Pro Ala Leu Glu Asn Arg Ala Ala Pro Ser Leu Ala Asp Asn

1090

1095

1100

aca aaa tcc ttc gac att ctc ttg gcc gaa gat aac atc gtc aat caa 3360

Thr Lys Ser Phe Asp Ile Leu Leu Ala Glu Asp Asn Ile Val Asn Gln

1105

1110

1115

1120

cgc tta gcg gtg aag att cta gaa aag tat cac cac gtc gtc aca gtc 3408

Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val

1125

1130

1135

gtt ggc aat ggt caa gaa gca cta gat gct atc aag gag aaa cga tac 3456

Val Gly Asn Gly Gln Glu Ala Leu Asp Ala Ile Lys Glu Lys Arg Tyr

1140

1145

1150

gat gtt att ctc atg gac gtt caa atg cca att atg gga gga ttc gaa 3504

Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu

1155

1160

1165

gca acc gct aag att aga gag tac gaa cgg agt ctt gga acg caa aga 3552

Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg

1170

1175

1180

acg cct att atc gca ctt aca gca cac gct atg ttg ggt gat cgc gaa 3600

Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu

1185

1190

1195

1200

aaa tgt att caa gcc caa atg gat gaa tat ctt tct aag cct ctg aaa 3648

Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys

1205

1210

1215

caa aat cat ctt att cag acg atc ttg aaa tgt gca acc ctt gga ggt 3696

Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly

1220

1225

1230

gca ttg ctc gag aag ggt agg gag gtt agg caa tcc gct aat gaa gag 3744

Ala Leu Leu Glu Lys Gly Arg Glu Val Arg Gln Ser Ala Asn Glu Glu

1235

1240

1245

agc ccc aat tcg caa aat ggt cct cgc ggt aca cag cat cct gca tca 3792

Ser Pro Asn Ser Gln Asn Gly Pro Arg Gly Thr Gln His Pro Ala Ser

1250

1255

1260

agt ccc aca cca gcc cat atg aga ccg gct atc gaa cct cgt gca tac 3840

Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr

1265

1270

1275

1280

acg acc act ggc cct ata aat cat gga agt gca gag agt cct tca ctt 3888

Thr Thr Thr Gly Pro Ile Asn His Gly Ser Ala Glu Ser Pro Ser Leu

1285

1290

1295

gta acg gca gat gct gag gat cca ctt gcg agg ctt cta atg cgt gcg 3936

Val Thr Ala Asp Ala Glu Asp Pro Leu Ala Arg Leu Leu Met Arg Ala

1300

1305

1310

cat agc agc tag

3948

His Ser Ser

1315

<210> 3

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 3

tattcagaga ctagtatgga ggattctaca atagca

36

<210> 4

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for PCR

<400> 4

cagatgaatc tgcagctagc tgctatgcgc acg

33

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 5

gatgtactca ctggtgcccc atcccgagcc

30

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for sequencing

<400> 6

ctcaaacagt tgagcatgta caccggccag

30

<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 7

acagaaggta ttctcggtgg acaagccaag

30

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for sequencing

<400> 8

gctagggagg tcggtaccga aggtagactg

30

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 9

atcttctcca acgaagtgca aagagtcgcc

30

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for sequencing

<400> 10

gaggagattc catacactct tagaggaacc

30

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 11

atcgacaaaag gacagactgg ccatggc

27

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for sequencing

<400> 12

atgccaatta tgggaggatt cgaagcaacc

30

<210> 13

<211> 1315

<212> PRT

<213> Botryotinia fuckeliana

<400> 13

Met Glu Asp Ser Thr Ile Ala His Thr Thr Ala Ile Leu Gln Thr Leu

1 5 10 15

Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys

20 25 30

Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu

35 40 45

Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg

50 55 60

Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu

65 70 75 80

Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg

85 90 95

Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu

100 105 110

Ala	Ala	Arg	Glu	Ala	Pro	Thr	Gly	Gly	Glu	Arg	Pro	Pro	Lys	Phe	Thr
115				120				125							
Lys	Leu	Ser	Asp	Glu	Glu	Leu	Glu	Ala	Leu	Arg	Glu	His	Val	Asp	His
130				135				140							
Gln	Ser	Lys	Gln	Leu	Asp	Ser	Gln	Lys	Ser	Glu	Leu	Ala	Gly	Val	His
145				150				155				160			
Ala	Gln	Leu	Phe	Glu	Gln	Lys	Gln	Arg	Gln	Glu	Gln	Ala	Leu	Asn	Val
165				170				175							
Leu	Glu	Val	Glu	Arg	Val	Ala	Ala	Leu	Glu	Arg	Glu	Leu	Lys	Lys	His
180				185				190							
Gln	Gln	Ala	Asn	Glu	Ala	Phe	Gln	Lys	Ala	Leu	Arg	Glu	Ile	Gly	Glu
195				200				205							
Ile	Val	Thr	Ala	Val	Ala	Arg	Gly	Asp	Leu	Ser	Lys	Lys	Val	Gln	Ile
210				215				220							
His	Ser	Val	Glu	Met	Asp	Pro	Glu	Ile	Thr	Thr	Phe	Lys	Arg	Val	Ile
225				230				235				240			
Asn	Thr	Met	Met	Asp	Gln	Leu	Gln	Ile	Phe	Ser	Ser	Glu	Val	Ser	Arg
245				250				255							
Val	Ala	Arg	Glu	Val	Gly	Thr	Glu	Gly	Ile	Leu	Gly	Gly	Gln	Ala	Lys
260				265				270							
Ile	Ser	Gly	Val	Asp	Gly	Thr	Trp	Lys	Glu	Leu	Thr	Asp	Asn	Val	Asn
275				280				285							
Val	Met	Ala	Gln	Asn	Leu	Thr	Asp	Gln	Val	Arg	Glu	Ile	Ala	Ser	Val
290				295				300							
Thr	Thr	Ala	Val	Ala	His	Gly	Asp	Leu	Thr	Gln	Lys	Ile	Glu	Arg	Pro
305				310				315				320			

Ala Gln Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val			
	325	330	335
Asp Gln Leu Arg Thr Phe Ala Ala Glu Val Thr Arg Val Ala Arg Asp			
	340	345	350
Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Glu Ser Glu Gly Val			
	355	360	365
Gln Gly Met Trp Asn Thr Leu Ile Val Asn Val Asn Ala Met Ala Asn			
	370	375	380
Asn Leu Thr Thr Gln Val Arg Asp Ile Ala Ile Val Thr Thr Ala Val			
	385	390	395
Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Lys Gly Glu			
	405	410	415
Ile Lys Gln Leu Lys Glu Thr Ile Asn Ser Met Val Asp Gln Leu Gln			
	420	425	430
Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu			
	435	440	445
Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly Thr Trp			
	450	455	460
Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr			
	465	470	475
Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Arg Gly Asp			
	485	490	495
Leu Thr Lys Lys Ile Glu Val Glu Val Gln Gly Glu Ile Ala Ser Leu			
	500	505	510
Lys Asp Thr Ile Asn Thr Met Val Asp Arg Leu Ser Thr Phe Ala Phe			
	515	520	525

Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly			
530	535	540	
Gly Gln Ala Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr			
545	550	555	560
Glu Asn Val Asn Thr Met Ala Arg Asn Leu Thr Thr Gln Val Arg Gly			
	565	570	575
Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Gln Lys			
	580	585	590
Ile Glu Val Ala Ala Ala Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile			
	595	600	605
Asn Asn Met Val Asp Arg Leu Ser Ile Phe Ser Asn Glu Val Gln Arg			
	610	615	620
Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln Ala Asp			
625	630	635	640
Val Ala Gly Ile Gly Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn			
	645	650	655
Thr Met Ala Asn Asn Leu Thr Thr Gln Val Arg Ala Phe Gly Asp Ile			
	660	665	670
Thr Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Ile Thr Val Glu			
	675	680	685
Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val			
	690	695	700
Tyr Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Leu Ala Arg Glu Ala			
705	710	715	720
Ala Glu Phe Ala Asn Arg Thr Lys Ser Glu Phe Leu Ala Asn Met Ser			
	725	730	735

His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu			
740	745	750	
Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile			
755	760	765	
Val His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu			
770	775	780	
Asp Leu Ser Lys Ile Glu Ala Asn Arg Met Ile Met Glu Glu Ile Pro			
785	790	795	800
Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val			
805	810	815	
Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser			
820	825	830	
Val Pro Asp His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Val Ile			
835	840	845	
Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val			
850	855	860	
Ser Leu Thr Ile Gln Lys Ala Glu Gln Asp His Cys Ala Pro Asn Glu			
865	870	875	880
Tyr Ala Val Glu Phe Cys Val Ser Asp Thr Gly Ile Gly Ile Gln Ala			
885	890	895	
Asp Lys Leu Asn Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser			
900	905	910	
Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys			
915	920	925	
Arg Leu Val Asn Leu Met Arg Gly Asp Val Trp Val Lys Ser Gln Tyr			
930	935	940	

Gly	Lys	Gly	Ser	Ser	Phe	Tyr	Phe	Thr	Cys	Thr	Val	Arg	Leu	Ala	Thr
945					950					955					960
Ser	Asp	Ile	Ser	Phe	Ile	Gln	Lys	Gln	Leu	Lys	Pro	Tyr	Gln	Gly	His
				965						970					975
Asn	Val	Leu	Phe	Ile	Asp	Lys	Gly	Gln	Thr	Gly	His	Gly	Lys	Glu	Ile
				980						985					990
Ile	Thr	Met	Leu	Thr	Gln	Leu	Gly	Leu	Val	Pro	Val	Val	Val	Asp	Ser
				995						1000					1005
Glu	Gln	His	Thr	Ile	Leu	Leu	Gly	Asn	Gly	Arg	Thr	Lys	Glu	Lys	Ile
				1010						1015					1020
Ala	Ser	Thr	Tyr	Asp	Val	Ile	Val	Val	Asp	Ser	Ile	Glu	Ser	Ala	Arg
1025					1030						1035				1040
Lys	Leu	Arg	Ser	Ile	Asp	Glu	Phe	Lys	Tyr	Ile	Pro	Ile	Val	Leu	Leu
					1045						1050				1055
Ala	Pro	Val	Ile	His	Val	Ser	Leu	Lys	Ser	Ala	Leu	Asp	Leu	Gly	Ile
				1060							1065				1070
Thr	Ser	Tyr	Met	Thr	Thr	Pro	Cys	Leu	Thr	Ile	Asp	Leu	Gly	Asn	Gly
				1075							1080				1085
Met	Ile	Pro	Ala	Leu	Glu	Asn	Arg	Ala	Ala	Pro	Ser	Leu	Ala	Asp	Asn
				1090							1095				1100
Thr	Lys	Ser	Phe	Asp	Ile	Leu	Leu	Ala	Glu	Asp	Asn	Ile	Val	Asn	Gln
1105					1110						1115				1120
Arg	Leu	Ala	Val	Lys	Ile	Leu	Glu	Lys	Tyr	His	His	Val	Val	Thr	Val
					1125						1130				1135
Val	Gly	Asn	Gly	Gln	Glu	Ala	Leu	Asp	Ala	Ile	Lys	Glu	Lys	Arg	Tyr
					1140						1145				1150

Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu			
1155	1160	1165	
Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg			
1170	1175	1180	
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu			
1185	1190	1195	1200
Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys			
1205	1210	1215	
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly			
1220	1225	1230	
Ala Leu Leu Glu Lys Gly Arg Glu Val Arg Gln Ser Ala Asn Glu Glu			
1235	1240	1245	
Ser Pro Asn Ser Gln Asn Gly Pro Arg Gly Thr Gln His Pro Ala Ser			
1250	1255	1260	
Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr			
1265	1270	1275	1280
Thr Thr Thr Gly Pro Ile Asn His Gly Ser Ala Glu Ser Pro Ser Leu			
1285	1290	1295	
Val Thr Ala Asp Ala Glu Asp Pro Leu Ala Arg Leu Leu Met Arg Ala			
1300	1305	1310	
His Ser Ser			
1315			

<210> 14

<211> 3948

<212> DNA

<213> Botryotinia fuckeliana

<220>

<221> CDS

<222> (1).. (3948)

<400> 14

atg gag gat tct aca ata gct cat act act gcg atc ctg caa act ctc 48

Met Glu Asp Ser Thr Ile Ala His Thr Thr Ala Ile Leu Gln Thr Leu

1 5 10 15

gca tta tcg agc atc gat ctt cca ctg acg aat gtt tac ggc aac aag 96

Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys

20 25 30

ggg att agg tta cca ggt gca gat acg gca gag aag ctt gcc ctc gaa 144

Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu

35 40 45

cga gaa ctt gcg gcc ttg gta tcc aga gtc caa aga tta gaa gca agg 192

Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg

50 55 60

gcg atc aca gtc aat aat caa acc ctg ccc gat acg ccg aat gaa tta 240

Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu

65	70	75	80	
gga gcg cca tct gct ttc gca gat gta ctc act ggt gcc cca tcc cga				288
Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg				
	85	90	95	
gcc tca aag agt act aca tcc cga caa cag ctc gta aat tcg ttg ctt				336
Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu				
	100	105	110	
gcc gcc aga gaa gcg ccc acc ggc ggt gaa aga cct cct aaa ttt acg				384
Ala Ala Arg Glu Ala Pro Thr Gly Gly Glu Arg Pro Pro Lys Phe Thr				
	115	120	125	
aaa tta agt gac gag gaa ctc gaa gca ctc cgc gaa cat gtc gac cat				432
Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His				
	130	135	140	
caa tcg aaa caa ctc gat agt caa aaa tct gag ctg gcc ggt gta cat				480
Gln Ser Lys Gln Leu Asp Ser Gln Lys Ser Glu Leu Ala Gly Val His				
145	150	155	160	
gct caa ctg ttt gag cag aag cag aga caa gaa caa gca ctc aac gtt				528
Ala Gln Leu Phe Glu Gln Lys Gln Arg Gln Glu Gln Ala Leu Asn Val				
	165	170	175	

ctt gaa gtc gaa cgc gta gca gct ctc gaa aga gaa ctg aag aag cat 576
 Leu Glu Val Glu Arg Val Ala Ala Leu Glu Arg Glu Leu Lys Lys His

180

185

190

caa caa gcc aac gag gct ttc caa aaa gct cta cgg gaa ata gga gag 624
 Gln Gln Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu

195

200

205

att gtc aca gct gta gct agg ggt gat ctc agt aag aag gta caa atc 672
 Ile Val Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Gln Ile

210

215

220

cac tcc gtg gag atg gac cct gag att aca act ttc aag cgt gtt att 720
 His Ser Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Val Ile

225

230

235

240

aat act atg atg gat caa ctt cag ata ttc tct agt gag gtt tct cgt 768
 Asn Thr Met Met Asp Gln Leu Gln Ile Phe Ser Ser Glu Val Ser Arg

245

250

255

gta gct aga gag gtc ggc aca gaa ggt att ctc ggt gga caa gcc aag 816
 Val Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Lys

260

265

270

att tct ggt gtt gat ggt aca tgg aag gag ttg act gac aat gtc aac 864
 Ile Ser Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn

275	280	285	
gtt atg gca caa aat ctc acc gat caa gtc cga gaa att gct tcc gtc			912
Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val			
290	295	300	
act act gct gta gct cat gga gat ctc aca caa aag att gag aga cca			960
Thr Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Arg Pro			
305	310	315	320
gcc cag ggt gag ata ctc caa ctg caa caa act atc aat acc atg gtg			1008
Ala Gln Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val			
	325	330	335
gat caa ttg aga acg ttc gcc gcc gag gtc acc cgc gta gca aga gat			1056
Asp Gln Leu Arg Thr Phe Ala Ala Glu Val Thr Arg Val Ala Arg Asp			
340	345	350	
gta gga act gaa ggt att ctt ggg ggt caa gca gaa agc gaa ggc gtc			1104
Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Glu Ser Glu Gly Val			
355	360	365	
cag ggc atg tgg aac aca ttg ata gtg aac gtc aac gct atg gcc aat			1152
Gln Gly Met Trp Asn Thr Leu Ile Val Asn Val Asn Ala Met Ala Asn			
370	375	380	

aac ctc acc aca caa gtg cgc gat ata gcc att gtc aca aca gct gtc	1200
Asn Leu Thr Thr Gln Val Arg Asp Ile Ala Ile Val Thr Thr Ala Val	
385 390 395 400	
gca aag gga gac ctg act caa aag gtc caa gca gaa tgt aag ggt gaa	1248
Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Lys Gly Glu	
405 410 415	
atc aag cag ttg aag gag act ata aat tcc atg gtg gac caa tta caa	1296
Ile Lys Gln Leu Lys Glu Thr Ile Asn Ser Met Val Asp Gln Leu Gln	
420 425 430	
caa ttt gcg cga gaa gtc acg aag att gct agg gag gtc ggt acc gaa	1344
Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu	
435 440 445	
ggt aga ctg ggt gga caa gca aca gtg cat gat gtt gaa ggc act tgg	1392
Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly Thr Trp	
450 455 460	
aga gac ctc acc gaa aat gtg aat ggt atg gcc atg aat ctt acg aca	1440
Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr	
465 470 475 480	
caa gta cga gag att gca aag gtt acc acc gct gtc gcc aga gga gat	1488
Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Arg Gly Asp	

485	490	495	
ttg acc aag aag att gaa gtc gag gtt cag gga gaa atc gct tcg ctg			1536
Leu Thr Lys Lys Ile Glu Val Glu Val Gln Gly Glu Ile Ala Ser Leu			
500	505	510	
aaa gat acc atc aac acc atg gtg gac aga ctt agt aca ttc gct ttt			1584
Lys Asp Thr Ile Asn Thr Met Val Asp Arg Leu Ser Thr Phe Ala Phe			
515	520	525	
gag gtt agc aaa gtc gcc agg gag gtc gga act gat ggg act ctt ggt			1632
Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly			
530	535	540	
gga caa gcg caa gtt gat aac gtc gaa gga aag tgg aaa gac ctc act			1680
Gly Gln Ala Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr			
545	550	555	560
gaa aat gtg aac acc atg gcc aga aac ttg act act caa gta cga ggt			1728
Glu Asn Val Asn Thr Met Ala Arg Asn Leu Thr Thr Gln Val Arg Gly			
565	570	575	
atc tcg act gtt aca caa gct att gcc aat gga gac atg agt cag aag			1776
Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Gln Lys			
580	585	590	

att gag gtt gct gct gcg ggt gaa ata ctc ata cta aag gaa acc ata 1824
 Ile Glu Val Ala Ala Ala Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile

595

600

605

aat aac atg gta gac aga ttg agt atc ttc tcc aac gaa gtg caa aga 1872
 Asn Asn Met Val Asp Arg Leu Ser Ile Phe Ser Asn Glu Val Gln Arg

610

615

620

gtc gcc aaa gat gtg ggt gtg gat ggt aag atg ggt ggc caa gct gac 1920
 Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln Ala Asp

625

630

635

640

gtt gct ggg att ggc ggc cgt tgg aaa gag atc aca acg gat gtc aat 1968
 Val Ala Gly Ile Gly Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn

645

650

655

acc atg gct aac aac ttg aca acc caa gtg cgc gcc ttt ggt gat ata 2016
 Thr Met Ala Asn Asn Leu Thr Thr Gln Val Arg Ala Phe Gly Asp Ile

660

665

670

act aac gcc gca acc gat ggc gac ttc aca aaa ttg atc act gtc gag 2064
 Thr Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Ile Thr Val Glu

675

680

685

gca tct gga gag atg gat gag ctg aag cga aag atc aac cag atg gtg 2112
 Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val

690	695	700	
tac aat ctg agg gac agt att caa aga aac acc ttg gct agg gag gct			2160
Tyr Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Leu Ala Arg Glu Ala			
705	710	715	720
gcc gaa ttc gcc aat agg acg aag tct gaa ttc ttg gct aac atg tct			2208
Ala Glu Phe Ala Asn Arg Thr Lys Ser Glu Phe Leu Ala Asn Met Ser			
	725	730	735
cac gag att cga aca cct atg aac ggt atc att ggt atg act cag ttg			2256
His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu			
	740	745	750
aca ctc gac acc gat ctt act caa tat caa cga gaa atg ctc aac att			2304
Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile			
	755	760	765
gtt cac aac ttg gcc aac agt tta ttg acc atc att gat gat att ctc			2352
Val His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu			
	770	775	780
gat tta tca aag atc gaa gca aac cgt atg atc atg gag gag att cca			2400
Asp Leu Ser Lys Ile Glu Ala Asn Arg Met Ile Met Glu Glu Ile Pro			
785	790	795	800

tac act ctt aga gga acc gtc ttc aac gcc ctc aag act ctc gct gtc	2448
Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val	
805 810 815	
aag gca aat gag aag ttc cta gac ctc act tac cgc gta gat agc tca	2496
Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser	
820 825 830	
gtt cca gat cac gtg gtt ggt gat tca ttc cgt ctt cga caa gtt att	2544
Val Pro Asp His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Val Ile	
835 840 845	
ctc aac ttg gtt gga aac gct atc aag ttc aca gag cat ggt gaa gtt	2592
Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val	
850 855 860	
tcg ttg acc atc caa aaa gcc gag caa gat cat tgt gcg ccg aac gaa	2640
Ser Leu Thr Ile Gln Lys Ala Glu Gln Asp His Cys Ala Pro Asn Glu	
865 870 875 880	
tat gca gtc gag ttt tgt gtt tct gac act ggt atc ggt atc caa gct	2688
Tyr Ala Val Glu Phe Cys Val Ser Asp Thr Gly Ile Gly Ile Gln Ala	
885 890 895	
gat aag ctc aat ttg att ttc gac act ttc caa caa gct gac gga tct	2736
Asp Lys Leu Asn Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser	

900	905	910	
atg acg agg aaa ttc gga ggt act ggt cta ggt cta tca att tcg aag			2784
Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys			
915	920	925	
aga ctt gta aac ctc atg cgt gga gat gtt tgg gtt aag agt cag tac			2832
Arg Leu Val Asn Leu Met Arg Gly Asp Val Trp Val Lys Ser Gln Tyr			
930	935	940	
gga aaa ggc agt tca ttc tac ttc acg tgt acc gtc cgc ctc gca acc			2880
Gly Lys Gly Ser Ser Phe Tyr Phe Thr Cys Thr Val Arg Leu Ala Thr			
945	950	955	960
tca gat atc agt ttc att cag aaa caa ctc aag cca tat caa ggt cac			2928
Ser Asp Ile Ser Phe Ile Gln Lys Gln Leu Lys Pro Tyr Gln Gly His			
965	970	975	
aat gtt ttg ttt atc gac aaa gga cag act ggc cat ggc aaa gaa ata			2976
Asn Val Leu Phe Ile Asp Lys Gly Gln Thr Gly His Gly Lys Glu Ile			
980	985	990	
atc act atg ctt aca caa ctt ggt ttg gta ccc gtt gtt gtt gac tct			3024
Ile Thr Met Leu Thr Gln Leu Gly Leu Val Pro Val Val Val Asp Ser			
995	1000	1005	

gag cag cac act att ctt ctc ggc aat gga aga acc aag gag aag att	3072
Glu Gln His Thr Ile Leu Leu Gly Asn Gly Arg Thr Lys Glu Lys Ile	
1010 1015 1020	
gct tca act tat gac gtg att gtt gtg gac tca att gag tcc gct cga	3120
Ala Ser Thr Tyr Asp Val Ile Val Val Asp Ser Ile Glu Ser Ala Arg	
1025 1030 1035 1040	
aaa ctg cga tca atc gat gag ttc aag tat att cca att gtt ctc tta	3168
Lys Leu Arg Ser Ile Asp Glu Phe Lys Tyr Ile Pro Ile Val Leu Leu	
1045 1050 1055	
gct ccc gtt att cat gtc agc tta aag tct gct ttg gat ctt ggt atc	3216
Ala Pro Val Ile His Val Ser Leu Lys Ser Ala Leu Asp Leu Gly Ile	
1060 1065 1070	
act tct tac atg acc act cca tgt tta acg atc gat ctt ggc aat ggt	3264
Thr Ser Tyr Met Thr Thr Pro Cys Leu Thr Ile Asp Leu Gly Asn Gly	
1075 1080 1085	
atg att cct gct ttg gag aat cga gct gca ccc tca ttg gcg gac aac	3312
Met Ile Pro Ala Leu Glu Asn Arg Ala Ala Pro Ser Leu Ala Asp Asn	
1090 1095 1100	
aca aaa tcc ttc gac att ctc ttg gcc gaa gat aac atc gtc aat caa	3360
Thr Lys Ser Phe Asp Ile Leu Leu Ala Glu Asp Asn Ile Val Asn Gln	

1105	1110	1115	1120	
cgc tta gcg gtg aag att cta gaa aag tat cac cac gtc gtc aca gtc				3408
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val				
	1125	1130	1135	
gtt ggc aat ggt caa gaa gca cta gat gct atc aag gag aaa cga tac				3456
Val Gly Asn Gly Gln Glu Ala Leu Asp Ala Ile Lys Glu Lys Arg Tyr				
	1140	1145	1150	
gat gtt att ctc atg gac gtt caa atg cca att atg gga gga ttc gaa				3504
Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu				
	1155	1160	1165	
gca acc gct aag att aga gag tac gaa cgg agt ctt gga acg caa aga				3552
Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg				
	1170	1175	1180	
acg cct att atc gca ctt aca gca cac gct atg ttg ggt gat cgc gaa				3600
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu				
1185	1190	1195	1200	
aaa tgt att caa gcc caa atg gat gaa tat ctt tct aag cct ctg aaa				3648
Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys				
	1205	1210	1215	

caa aat cat ctt att cag acg atc ttg aaa tgt gca acc ctt gga ggt	3696
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly	
1220 1225 1230	
gca ttg ctc gag aag ggt agg gag gtt agg caa tcc gct aat gaa gag	3744
Ala Leu Leu Glu Lys Gly Arg Glu Val Arg Gln Ser Ala Asn Glu Glu	
1235 1240 1245	
agc ccc aat tcg caa aat ggt cct cgc ggt aca cag cat cct gca tca	3792
Ser Pro Asn Ser Gln Asn Gly Pro Arg Gly Thr Gln His Pro Ala Ser	
1250 1255 1260	
agt ccc aca cca gcc cat atg aga ccg gct atc gaa cct cgt gca tac	3840
Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr	
1265 1270 1275 1280	
acg acc act ggc cct ata aat cat gga agt gca gag agt cct tca ctt	3888
Thr Thr Thr Gly Pro Ile Asn His Gly Ser Ala Glu Ser Pro Ser Leu	
1285 1290 1295	
gta acg gca gat gct gag gat cca ctt gcg agg ctt cta atg cgt gcg	3936
Val Thr Ala Asp Ala Glu Asp Pro Leu Ala Arg Leu Leu Met Arg Ala	
1300 1305 1310	
cat agc agc tag	3948
His Ser Ser	

1315

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 15

ggtcaagcag aaagcgaagg cgtccagggc

30

<210> 16

<211> 1307

<212> PRT

<213> Magnapotrthe grisea

<400> 16

Met Ala Asp Ala Ala Thr Leu Ala Ala Val Ala Ala Ile Val Glu Asn

1

5

10

15

Ile Ala Thr Asn Ser Gly Ala Pro Gly Lys Asn Ala Ser Phe Arg Ser

20

25

30

Ser Thr Tyr Val Gln Leu Pro Gly Pro Glu Ser Asp Glu Lys Lys Gln			
35	40	45	
Leu Glu Arg Glu Leu Ala Ala Leu Val Ile Arg Val Gln Gln Leu Glu			
50	55	60	
Thr Arg Ala Asn Ala Ala Pro Ala Thr Ile Phe Pro Asp Thr Pro Asn			
65	70	75	80
Glu Thr Ala His Ser Leu Phe Gly Asp Asp Ser Ser Ser Pro Thr Ser			
85	90	95	
Ser Ser Ser Gly Arg Glu Pro Lys Arg Leu Lys Ser Ala Ser Ser Thr			
100	105	110	
Thr Arg Asn Gly Phe Thr Thr Asp Gly Arg Pro Ser Lys Leu Asn Ala			
115	120	125	
Ile Thr Asp Glu Glu Leu Glu Gly Leu Arg Glu His Val Asp Gly Gln			
130	135	140	
Ser Arg Leu Leu Asp Ser Gln Arg Ala Glu Leu Asp Gly Val Asn Ala			
145	150	155	160
Gln Leu Leu Glu Gln Lys Gln Leu Gln Glu Arg Ala Leu Ala Ile Ile			
165	170	175	
Glu Gln Glu Arg Val Ala Thr Leu Glu Arg Glu Leu Trp Lys His Gln			
180	185	190	
Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Ser Ile			
195	200	205	
Val Thr Ala Ala Ala Arg Gly Asp Leu Ser Lys Arg Val Lys Ile Asn			
210	215	220	
Pro Ile Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Thr Met Asn			
225	230	235	240

Ala Met Met Asp Gln Leu Gly Val Phe Ser Ser Glu Val Ser Arg Val			
	245	250	255
Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Gln Ile			
	260	265	270
Glu Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn Val			
	275	280	285
Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val Thr			
	290	295	300
Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Ser Ala Ala			
	305	310	315
Lys Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val Asp			
	325	330	335
Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala Arg Asp Val			
	340	345	350
Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Glu Gly Val Lys			
	355	360	365
Gly Met Trp Asn Glu Leu Thr Val Asn Val Asn Ala Met Ala Asn Asn			
	370	375	380
Leu Thr Thr Gln Val Arg Asp Ile Ile Asn Val Thr Thr Ala Val Ala			
	385	390	395
Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Arg Gly Glu Ile			
	405	410	415
Phe Glu Leu Lys Asn Thr Ile Asn Ser Met Val Asp Gln Leu Gln Gln			
	420	425	430
Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu Gly			
	435	440	445

Arg	Leu	Gly	Gly	Gln	Ala	Thr	Val	His	Asp	Val	Gln	Gly	Thr	Trp	Arg
450							455							460	
Asp	Leu	Thr	Glu	Asn	Val	Asn	Gly	Met	Ala	Met	Asn	Leu	Thr	Thr	Gln
465						470					475				480
Val	Arg	Glu	Ile	Ala	Asn	Val	Thr	Ser	Ala	Val	Ala	Ala	Gly	Asp	Leu
					485					490					495
Ser	Lys	Lys	Ile	Arg	Val	Glu	Val	Lys	Gly	Glu	Ile	Leu	Asp	Leu	Lys
					500					505					510
Asn	Thr	Ile	Asn	Thr	Met	Val	Asp	Arg	Leu	Gly	Thr	Phe	Ala	Phe	Glu
			515						520					525	
Val	Ser	Lys	Val	Ala	Arg	Ala	Val	Gly	Thr	Asp	Gly	Thr	Leu	Gly	Gly
			530						535					540	
Gln	Ala	Gln	Val	Glu	Asn	Val	Glu	Gly	Lys	Trp	Lys	Asp	Leu	Thr	Glu
545						550					555				560
Asn	Val	Asn	Thr	Met	Ala	Ser	Asn	Leu	Thr	Ser	Gln	Val	Arg	Gly	Ile
					565					570					575
Ser	Thr	Val	Thr	Gln	Ala	Ile	Ala	Asn	Gly	Asp	Met	Ser	Arg	Lys	Ile
					580					585					590
Asp	Val	Glu	Ala	Lys	Gly	Glu	Ile	Leu	Ile	Leu	Lys	Glu	Thr	Ile	Asn
					595					600					605
Asn	Met	Val	Asp	Arg	Leu	Ser	Ile	Phe	Cys	Asn	Glu	Val	Gln	Arg	Val
					610					615					620
Ala	Lys	Asp	Val	Gly	Val	Asp	Gly	Ile	Met	Gly	Gly	Gln	Ala	Asp	Val
625										630					635
Ala	Gly	Leu	Lys	Gly	Arg	Trp	Lys	Glu	Ile	Thr	Thr	Asp	Val	Asn	Thr
										645					650
															655

Met Ala Asn Asn Leu Thr Ala Gln Val Arg Ala Phe Gly Asp Ile Thr			
660	665	670	
Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Glu Val Glu Ala			
675	680	685	
Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val Tyr			
690	695	700	
Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg Glu Ala Ala			
705	710	715	720
Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn Met Ser His			
725	730	735	
Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu Thr			
740	745	750	
Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile Val			
755	760	765	
Asn Asn Leu Ala Met Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp			
770	775	780	
Leu Ser Lys Ile Glu Ala Lys Arg Met Val Ile Glu Glu Ile Pro Tyr			
785	790	795	800
Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys			
805	810	815	
Ala Asn Asp Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser Val			
820	825	830	
Pro Asp His Val Ile Gly Asp Ser Phe Arg Leu Arg Gln Ile Ile Leu			
835	840	845	
Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val Ser			
850	855	860	

Leu Thr Ile Gln Lys Gly Asn Asp Val Thr Cys Leu Pro Asn Glu Tyr			
865	870	875	880
Met Ile Glu Phe Val Val Ser Asp Thr Gly Ile Gly Ile Pro Thr Asp			
	885	890	895
Lys Leu Gly Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser Met			
	900	905	910
Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg			
	915	920	925
Leu Val Asn Leu Met Gly Gly Asp Val Trp Val Lys Ser Gln Tyr Gly			
	930	935	940
Lys Gly Ser Ser Phe Tyr Phe Thr Cys Arg Val Arg Leu Ala Asp Val			
945	950	955	960
Asp Ile Ser Leu Ile Arg Lys Gln Leu Lys Pro Tyr Lys Gly His Gln			
	965	970	975
Val Leu Phe Ile Asp Lys Gly Lys Thr Gly His Gly Pro Glu Val Gly			
	980	985	990
Gln Met Leu Gly Gln Leu Gly Leu Val Pro Ile Val Leu Glu Ser Glu			
	995	1000	1005
Gln Asn His Thr Leu Thr Arg Val Arg Gly Lys Glu Cys Pro Tyr Asp			
	1010	1015	1020
Val Ile Val Val Asp Ser Ile Asp Thr Ala Arg Arg Leu Arg Gly Ile			
1025	1030	1035	1040
Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu Ala Pro Thr Val His			
	1045	1050	1055
Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile Thr Ser Tyr Met Thr			
	1060	1065	1070

Met Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly Met Val Pro Ala Leu			
1075	1080	1085	
Glu Asn Arg Ala Thr Pro Ser Leu Ser Asp Asn Thr Lys Ser Phe Glu			
1090	1095	1100	
Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln Arg Leu Ala Val Lys			
1105	1110	1115	1120
Ile Leu Glu Lys Tyr Asn His Val Val Thr Val Val Ser Asn Gly Ala			
1125	1130	1135	
Glu Ala Leu Glu Ala Val Lys Asp Asn Lys Tyr Asp Val Ile Leu Met			
1140	1145	1150	
Asp Val Gln Met Pro Val Met Gly Gly Phe Glu Ala Thr Ala Lys Ile			
1155	1160	1165	
Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg Thr Pro Ile Ile Ala			
1170	1175	1180	
Leu Thr Ala His Ala Met Met Gly Asp Arg Glu Lys Cys Ile Glu Ala			
1185	1190	1195	1200
Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln Gln Asn His Leu Ile			
1205	1210	1215	
Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly Ala Leu Leu Glu Gln			
1220	1225	1230	
Asn Arg Glu Arg Glu Leu Glu Leu Ala Arg His Ala Glu His Lys Gly			
1235	1240	1245	
Gly Leu Ser Thr Asp Pro Ala Arg Ala Ser Ser Val Met Arg Pro Pro			
1250	1255	1260	
Leu His His Arg Pro Val Thr Thr Ala Glu Ser Leu Ser Gly Gly Ala			
1265	1270	1275	1280

Glu Ser Pro Ser Leu Met Ala Asn Asp Gly Glu Asp Pro Ile Gln Arg

1285

1290

1295

Ala Arg Ser Ser Leu Ser Glu Pro Gly Cys Leu

1300

1305

<210> 17

<211> 3924

<212> DNA

<213> Magnapotrthe grisea

<220>

<221> CDS

<222> (1).. (3924)

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Met Ala Asp Ala Ala Thr Leu Ala Ala Val Ala Ala Ile Val Glu Asn

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15

atc gct acc aac tcg ggg gcc cct gga aaa aat gct tca ttt cgc tcc 96

Ile Ala Thr Asn Ser Gly Ala Pro Gly Lys Asn Ala Ser Phe Arg Ser

20

25

30

agt acc tat gtc cag ctt ccc ggt ccg gaa tcc gac gag aag aaa cag 144

Ser Thr Tyr Val Gln Leu Pro Gly Pro Glu Ser Asp Glu Lys Lys Gln

35	40	45	
ctc gag cgc gag ctt gcc gcc ctg gtg ata agg gta cag cag ctc gaa			192
Leu Glu Arg Glu Leu Ala Ala Leu Val Ile Arg Val Gln Gln Leu Glu			
50	55	60	
acc cgt gcc aac ggc gct cct gct aca ata ttc ccc gac aca ccc aac			240
Thr Arg Ala Asn Ala Ala Pro Ala Thr Ile Phe Pro Asp Thr Pro Asn			
65	70	75	80
gaa act gca cat tca ctc ttt ggc gat gat agc tcg tcc cct acc agt			288
Glu Thr Ala His Ser Leu Phe Gly Asp Asp Ser Ser Ser Pro Thr Ser			
85	90	95	
tcg agc tca ggc cgg gag cct aaa cga ctg aag tcg gca tcc agc aca			336
Ser Ser Ser Gly Arg Glu Pro Lys Arg Leu Lys Ser Ala Ser Ser Thr			
100	105	110	
acg agg aat ggt ttc act acg gac ggt cgt cca tca aag ctc aac gca			384
Thr Arg Asn Gly Phe Thr Thr Asp Gly Arg Pro Ser Lys Leu Asn Ala			
115	120	125	
atc acc gat gag gag ctc gaa ggc ttg cgc gaa cat gtt gac ggc cag			432
Ile Thr Asp Glu Glu Leu Glu Gly Leu Arg Glu His Val Asp Gly Gln			
130	135	140	

tcc cgg ctg ctc gac agc caa agg gcc gag ctg gac ggc gtc aat gcc	480
Ser Arg Leu Leu Asp Ser Gln Arg Ala Glu Leu Asp Gly Val Asn Ala	
145 150 155 160	
caa ctc ttg gag cag aag cag ctg caa gag cgc gcc ctt gcc ata atc	528
Gln Leu Leu Glu Gln Lys Gln Leu Gln Glu Arg Ala Leu Ala Ile Ile	
165 170 175	
gag cag gaa cgt gta gcc act ttg gag aga gag cta tgg aaa cat caa	576
Glu Gln Glu Arg Val Ala Thr Leu Glu Arg Glu Leu Trp Lys His Gln	
180 185 190	
aag gcc aac gag gcc ttc cag aag gct ctc cgg gag att gga tcg ata	624
Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Ser Ile	
195 200 205	
gtg acc gct gca gcc cgg ggt gac ctc tct aag agg gtc aag ata aac	672
Val Thr Ala Ala Ala Arg Gly Asp Leu Ser Lys Arg Val Lys Ile Asn	
210 215 220	
cgc att gag atg gac cct gaa atc acc aca ttc aag agg acc atg aac	720
Pro Ile Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Thr Met Asn	
225 230 235 240	
gcc atg atg gat caa ctt ggc gtc ttc tct agt gaa gtc tcg cga gtg	768
Ala Met Met Asp Gln Leu Gly Val Phe Ser Ser Glu Val Ser Arg Val	

245	250	255	
gca aga gag gtc ggc acc gag ggc ata tta ggt gga cag gcc cag atc			816
Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Gln Ile			
260	265	270	
gag gga gtg gac ggc acg tgg aaa gaa ctg acg gac aat gtc aac gtc			864
Glu Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn Val			
275	280	285	
atg gcg cag aac ctg acc gac caa gtc cgc gaa atc gcc tca gtc act			912
Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val Thr			
290	295	300	
aca gct gtg gcc cac gga gat ttg acc caa aag att gag agt gcg gcc			960
Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Ser Ala Ala			
305	310	315	320
aag gga gaa atc cta cag ctt caa caa act ata aat acc atg gtg gac			1008
Lys Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val Asp			
325	330	335	
caa cta cgc aca ttt gct tca gag gtt acc cgt gtc gcc cgt gac gtc			1056
Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala Arg Asp Val			
340	345	350	

gga acc gag gga atg ctc ggc ggg cag gct gac gtt gaa ggg gtc aag	1104
Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Glu Gly Val Lys	
355 360 365	
ggc atg tgg aat gag ctg acg gtc aac gtc aac gcc atg gcc aac aat	1152
Gly Met Trp Asn Glu Leu Thr Val Asn Val Asn Ala Met Ala Asn Asn	
370 375 380	
tta aca acc caa gtg cgc gac atc atc aac gtt acc aca gcc gtc gca	1200
Leu Thr Thr Gln Val Arg Asp Ile Ile Asn Val Thr Thr Ala Val Ala	
385 390 395 400	
aag gga gat ctt aca caa aag gtg cag gcg gaa tgt cgc ggc gag att	1248
Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Arg Gly Glu Ile	
405 410 415	
ttt gag ctc aag aac acg atc aat tcc atg gtg gac cag ctg cag caa	1296
Phe Glu Leu Lys Asn Thr Ile Asn Ser Met Val Asp Gln Leu Gln Gln	
420 425 430	
ttt gct cgc gag gtt acc aag atc gcc aga gag gtt ggt acc gaa gga	1344
Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu Gly	
435 440 445	
cgg ctg ggc ggc caa gca act gtt cac gat gta cag gga act tgg cga	1392
Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Gln Gly Thr Trp Arg	

450	455	460	
gat ctc aca gaa aac gtg aac gga atg gct atg aat ctc acc aca caa			1440
Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr Gln			
465	470	475	480
gta cga gag ata gcc aat gtt acc agt gcc gtc gct gca ggc gac cta			1488
Val Arg Glu Ile Ala Asn Val Thr Ser Ala Val Ala Ala Gly Asp Leu			
	485	490	495
tcc aag aag atc agg gta gag gtc aag ggc gag att ctg gac ctc aaa			1536
Ser Lys Lys Ile Arg Val Glu Val Lys Gly Glu Ile Leu Asp Leu Lys			
	500	505	510
aat acc atc aac acc atg gtt gac cgc ctc gga act ttc gcc ttc gaa			1584
Asn Thr Ile Asn Thr Met Val Asp Arg Leu Gly Thr Phe Ala Phe Glu			
	515	520	525
gtc agc aaa gta gcc cga gcc gtc ggc aca gat ggc act ctt ggt ggt			1632
Val Ser Lys Val Ala Arg Ala Val Gly Thr Asp Gly Thr Leu Gly Gly			
530	535	540	
cag gct caa gtt gag aat gtg gag ggc aaa tgg aaa gac ctc acc gaa			1680
Gln Ala Gln Val Glu Asn Val Glu Gly Lys Trp Lys Asp Leu Thr Glu			
545	550	555	560

aac gtc aac acc atg gcg tca aac ctc act tct cag gtc agg gga ata 1728
 Asn Val Asn Thr Met Ala Ser Asn Leu Thr Ser Gln Val Arg Gly Ile

565

570

575

tca acc gtg aca caa gcc atc gcg aac ggt gac atg agc cga aag atc 1776
 Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Arg Lys Ile

580

585

590

gac gtg gaa gcc aag ggc gag ata cta atc ctc aag gaa act atc aac 1824
 Asp Val Glu Ala Lys Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile Asn

595

600

605

aac atg gtt gat cgt ctg tcg ata ttc tgc aat gaa gta caa cga gtc 1872
 Asn Met Val Asp Arg Leu Ser Ile Phe Cys Asn Glu Val Gln Arg Val

610

615

620

gca aaa gat gta ggc gtt gat ggc att atg ggg gga caa gcc gac gtt 1920
 Ala Lys Asp Val Gly Val Asp Gly Ile Met Gly Gly Gln Ala Asp Val

625

630

635

640

gca ggt ctc aag ggg cga tgg aag gag att acc acc gat gtc aac acc 1968
 Ala Gly Leu Lys Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn Thr

645

650

655

atg gcc aac aat ctt acg gcg caa gta cgc gct ttc gga gat ata acc 2016
 Met Ala Asn Asn Leu Thr Ala Gln Val Arg Ala Phe Gly Asp Ile Thr

660	665	670	
aat gcc gct acc gac gga gac ttc acc aag ctg gtc gag gtt gag gcg			2064
Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Glu Val Glu Ala			
675	680	685	
tcg ggc gaa atg gac gaa ctg aag cgc aag atc aat caa atg gtc tac			2112
Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val Tyr			
690	695	700	
aat ctc cga gac agt atc caa aga aac acg caa gca aga gaa gcc gca			2160
Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg Glu Ala Ala			
705	710	715	720
gaa ttg gcc aac aag acg aag tcg gag ttc ctc gct aac atg tcc cac			2208
Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn Met Ser His			
725	730	735	
gaa atc cgc aca ccc atg aac ggt atc atc ggc atg aca caa ctt act			2256
Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu Thr			
740	745	750	
ctt gat aca gat ttg acg caa tac caa cgc gaa atg ctc aac att gtc			2304
Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile Val			
755	760	765	

aac aat ctc gcc atg agt ctg ctc acc att atc gac gac atc ctc gat 2352

Asn Asn Leu Ala Met Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp

770

775

780

ctg tca aag att gag gct aag cgg atg gtt atc gag gag att cca tac 2400

Leu Ser Lys Ile Glu Ala Lys Arg Met Val Ile Glu Glu Ile Pro Tyr

785

790

795

800

acg tta cga gga acg gtc ttc aac gca ctg aag act ttg gcg gtc aag 2448

Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys

805

810

815

gcg aac gac aag ttt ttg gat ctc acg tac cgt gtg gac agc tca gtt 2496

Ala Asn Asp Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser Val

820

825

830

cct gac cac gtc atc ggt gac tcg ttc cgt ctg cgc cag att atc ctg 2544

Pro Asp His Val Ile Gly Asp Ser Phe Arg Leu Arg Gln Ile Ile Leu

835

840

845

aac ctg gtt ggc aat gcc atc aaa ttc acc gag cat gga gag gtc agc 2592

Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val Ser

850

855

860

ctt act atc cag aag ggc aac gac gtg acg tgc ctg cca aac gag tac 2640

Leu Thr Ile Gln Lys Gly Asn Asp Val Thr Cys Leu Pro Asn Glu Tyr

865	870	875	880	
atg atc gaa ttt gtc gtg tcg gac acg ggc ata gga att cca acg gac				2688
Met Ile Glu Phe Val Val Ser Asp Thr Gly Ile Gly Ile Pro Thr Asp				
	885	890	895	
aaa ctg ggt ctc atc ttc gac aca ttc cag cag gct gat gga tcc atg				2736
Lys Leu Gly Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser Met				
	900	905	910	
aca cgc aag ttt ggc gga acc ggg ctt ggt ctg tct att tcc aag agg				2784
Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg				
	915	920	925	
ctc gtc aac ctc atg ggc ggt gac gtg tgg gtc aag tca caa tac ggc				2832
Leu Val Asn Leu Met Gly Gly Asp Val Trp Val Lys Ser Gln Tyr Gly				
	930	935	940	
aag ggc agc tcg ttc tac ttc act tgt cgt gtc cgc ctc gcc gac gtg				2880
Lys Gly Ser Ser Phe Tyr Phe Thr Cys Arg Val Arg Leu Ala Asp Val				
945	950	955	960	
gat atc tca ctc atc agg aag cag ctg aag cct tac aag gga cac cag				2928
Asp Ile Ser Leu Ile Arg Lys Gln Leu Lys Pro Tyr Lys Gly His Gln				
	965	970	975	

gtc ctg ttc atc gat aag ggc aag act gga cac ggg ccc gag gtg ggg	2976
Val Leu Phe Ile Asp Lys Gly Lys Thr Gly His Gly Pro Glu Val Gly	
980 985 990	
cag atg ctc ggc cag ctg ggt ttg gtg ccc atc gtg ctg gaa tcc gag	3024
Gln Met Leu Gly Gln Leu Gly Leu Val Pro Ile Val Leu Glu Ser Glu	
995 1000 1005	
caa aat cac acc ctg acg cgg gtg cgc ggc aag gaa tgt ccc tac gac	3072
Gln Asn His Thr Leu Thr Arg Val Arg Gly Lys Glu Cys Pro Tyr Asp	
1010 1015 1020	
gtg ata gtt gtc gac tca atc gac aca gcc cgg cgc ctg aga gga att	3120
Val Ile Val Val Asp Ser Ile Asp Thr Ala Arg Arg Leu Arg Gly Ile	
1025 1030 1035 1040	
gac gac ttc aag tat ctg ccc atc gtt ctc ctg gcg cca act gtc cac	3168
Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu Ala Pro Thr Val His	
1045 1050 1055	
gtc agc ctg aaa tcc tgc ttg gac ttg ggt att acc tcg tat atg acg	3216
Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile Thr Ser Tyr Met Thr	
1060 1065 1070	
atg ccc tgc aag ctc atc gac ctc ggc aat ggt atg gtt ccc gct ctt	3264
Met Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly Met Val Pro Ala Leu	

1075	1080	1085	
gag aac cgt gcc aca cca tca cta tca gac aac act aag tcg ttc gaa			3312
Glu Asn Arg Ala Thr Pro Ser Leu Ser Asp Asn Thr Lys Ser Phe Glu			
1090	1095	1100	
att ctg ctg gcc gag gac aac acc gtc aac cag cgc ctg gcc gtt aag			3360
Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln Arg Leu Ala Val Lys			
1105	1110	1115	1120
att ctt gaa aag tac aac cac gtt gtg acg gta gtc agc aac ggt gct			3408
Ile Leu Glu Lys Tyr Asn His Val Val Thr Val Val Ser Asn Gly Ala			
	1125	1130	1135
gaa gct ctt gaa gct gtc aag gat aac aaa tac gat gtg atc ctg atg			3456
Glu Ala Leu Glu Ala Val Lys Asp Asn Lys Tyr Asp Val Ile Leu Met			
1140	1145	1150	
gat gtt caa atg cct gtc atg ggt gga ttt gag gcg acg gca aag att			3504
Asp Val Gln Met Pro Val Met Gly Gly Phe Glu Ala Thr Ala Lys Ile			
1155	1160	1165	
cgt gaa tac gag cgc agc ctg ggc aca cag agg aca cca atc atc gcg			3552
Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg Thr Pro Ile Ile Ala			
1170	1175	1180	

ctt acc gct cac gca atg atg ggc gac cgt gag aag tgt atc gag gcc	3600
Leu Thr Ala His Ala Met Met Gly Asp Arg Glu Lys Cys Ile Glu Ala	
1185 1190 1195 1200	
cag atg gac gag tac ctg tcg aag cct ctg cag cag aac cac ttg ata	3648
Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln Gln Asn His Leu Ile	
1205 1210 1215	
caa aca att ctc aag tgt gca acg ctg ggt ggc gcc ttg ttg gaa caa	3696
Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly Ala Leu Leu Glu Gln	
1220 1225 1230	
aat cgt gag cgc gag ctt gaa cta gca agg cat gcc gaa cac aaa gga	3744
Asn Arg Glu Arg Glu Leu Glu Leu Ala Arg His Ala Glu His Lys Gly	
1235 1240 1245	
gga ctg tct acg gac ccg gcg agg gca tcg tcg gta atg cgt ccg cca	3792
Gly Leu Ser Thr Asp Pro Ala Arg Ala Ser Ser Val Met Arg Pro Pro	
1250 1255 1260	
cta cac cac cga ccg gtg act aca gcc gag tcg ctt tct ggt ggc gcc	3840
Leu His His Arg Pro Val Thr Thr Ala Glu Ser Leu Ser Gly Gly Ala	
1265 1270 1275 1280	
gaa agc ccc tcg ttg atg gca aat gac ggc gaa gat cca ata caa agg	3888
Glu Ser Pro Ser Leu Met Ala Asn Asp Gly Glu Asp Pro Ile Gln Arg	

1285

1290

1295

gca cgt agc agt ctc tct gaa cca gga tgc cta taa

3924

Ala Arg Ser Ser Leu Ser Glu Pro Gly Cys Leu

1300

1305

<210> 18

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 18

acgactagta tggcggacgc cgcgactctg gcag

34

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 19

ctgaagcttt tataggcatc ctgtttcaga gaga

34

<210> 20

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for Sequencing

<400> 20

ttcactacgg acggtcgtcc atcaa

25

<210> 21

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 21

ttaggtggac aggcccagat cgagg

25

<210> 22

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 22

tcaagaacac gatcaattcc atggt

25

<210> 23

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 23

gtcaaacctc agcttctcag gtcag

25

<210> 24

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 24

ccaacaagac gaagtcggag ttcct

25

<210> 25

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 25

cgtgacgtgc ctgccaaacg agtac

25

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 26

atagttgtcg actcaatcga cacag

25

<210> 27

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 27

acagaggaca ccaatcatcg cgctt

25

<210> 28

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 28

gttttcccag tcacgac

17

<210> 29

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 29

caggaaacag ctatgac

17

<210> 30

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 30

aacatgtccc acgarattcg macacc

26

<210> 31

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 31

cacgagattc gvacacccat gaaygg

26

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 32

aggccttcca aaaggctctv cggga

25

<210> 33

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 33

gagatggacc ctgaaatcac mac

23

<210> 34

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 34

cagatattct cyagygaagt ytckcg

26

<210> 35

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 35

atagcrttgc caacmaggtt magaataa

28

<210> 36

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 36

aacttgatgg crttkccaac maggtt

26

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 37

ctctgtgaac ttgatrgcrt tkccaac

27

<210> 38

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 38

atacactttt cncggtcacc catcat

26

<210> 39

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 39

tccatctgbg cctggataca cttttc

26

<210> 40

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 40

ggcttv gava gatactcgtc catctg

26

<210> 41

<211> 1293

<212> PRT

<213> Fusarium oxysporum

<400> 41

Met	Val	Asp	Asp	Ala	Ala	Leu	Ala	Ala	Ala	Ala	Ser	Ile	Val	Ala	Ser
1				5						10				15	
Ile	Ala	Pro	Asp	Pro	Arg	Leu	Pro	Asn	Ser	Ile	Pro	Val	Gly	Val	Ala
				20					25					30	
Ser	Gln	Val	Gln	Leu	Pro	Gly	Pro	Asp	Thr	Pro	Ala	Lys	Arg	Lys	Leu
				35					40					45	
Glu	Leu	Glu	Leu	Gln	Asn	Leu	Ala	Leu	Arg	Val	Gly	Lys	Leu	Glu	Ser
				50				55					60		
Gln	Ala	Ser	Ala	Thr	Ser	Pro	Phe	Pro	Glu	Thr	Pro	Asn	Glu	Val	Ile
				65				70					75		80
Asp	Thr	Leu	Phe	Gly	Glu	Glu	Ala	Gln	Ala	Val	Ala	Val	Arg	Pro	Lys
								85					90		95
Pro	Lys	Val	Phe	His	Ala	Gln	Gly	Ser	Leu	His	Ser	Pro	His	Leu	Pro
				100					105					110	
Ser	Tyr	Gln	Leu	Thr	Glu	Glu	Ala	Leu	Glu	Gly	Leu	Arg	Glu	His	Val
				115				120					125		
Asp	Asp	Gln	Ser	Lys	Leu	Leu	Asp	Ser	Gln	Arg	Gln	Glu	Leu	Ala	Gly
				130				135					140		
Val	Asn	Ala	Gln	Leu	Leu	Glu	Gln	Lys	Gln	Leu	Gln	Glu	Arg	Ala	Leu
				145				150				155		160	
Glu	Ile	Leu	Glu	Gln	Glu	Arg	Ile	Ala	Thr	Leu	Glu	Arg	Glu	Leu	Trp
								165				170		175	
Lys	His	Gln	Lys	Ala	Asn	Glu	Ala	Phe	Gln	Lys	Ala	Leu	Arg	Glu	Ile
				180				185					190		
Gly	Glu	Ile	Val	Thr	Ala	Val	Ala	Arg	Gly	Asp	Leu	Thr	Met	Lys	Val
				195				200					205		

Arg Met Asn Thr Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg			
210	215	220	
Thr Ile Asn Ala Met Met Asp Gln Leu Gln Ile Phe Ala Ser Glu Val			
225	230	235	240
Ser Arg Val Ala Arg Glu Val Gly Thr Glu Gly Leu Leu Gly Gly Gln			
245	250	255	
Ala Arg Ile Gly Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn			
260	265	270	
Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala			
275	280	285	
Ser Val Thr Thr Ala Val Ala His Gly Asp Leu Thr Lys Lys Ile Glu			
290	295	300	
Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr			
305	310	315	320
Met Val Asp Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala			
325	330	335	
Arg Asp Val Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Gly			
340	345	350	
Gly Val Gln Gly Met Trp Asn Asp Leu Thr Val Asn Val Asn Ala Met			
355	360	365	
Ala Asn Asn Leu Thr Thr Gln Val Arg Asp Ile Ile Lys Val Thr Thr			
370	375	380	
Ala Val Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Asp Cys Arg			
385	390	395	400
Gly Glu Ile Phe Glu Leu Lys Ser Thr Ile Asn Ser Met Val Asp Gln			
405	410	415	

Leu Gln Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly
 420 425 430
 Thr Glu Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly
 435 440 445
 Thr Trp Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu
 450 455 460
 Thr Thr Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Lys
 465 470 475 480
 Gly Asp Leu Thr Lys Lys Ile Gly Val Glu Val Lys Gly Glu Ile Ala
 485 490 495
 Glu Leu Lys Asn Thr Ile Asn Gln Met Val Asp Arg Leu Gly Thr Phe
 500 505 510
 Ala Val Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr
 515 520 525
 Leu Gly Gly Gln Ala Gln Val Ala Asn Val Glu Gly Lys Trp Lys Asp
 530 535 540
 Leu Thr Glu Asn Val Asn Thr Met Ala Ser Asn Leu Thr Val Gln Val
 545 550 555 560
 Arg Ser Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser
 565 570 575
 Gln Lys Ile Lys Val Glu Ala Asn Gly Glu Ile Gln Val Leu Lys Glu
 580 585 590
 Thr Ile Asn Asn Met Val Asp Arg Leu Ser Ser Phe Cys Tyr Glu Val
 595 600 605
 Gln Arg Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Ala Gln
 610 615 620

Ala Asp Val Gly Gly Leu Asp Gly Arg Trp Lys Glu Ile Thr Thr Asp
 625 630 635 640
 Val Asn Thr Met Ala Ser Asn Leu Thr Thr Gln Val Arg Ala Phe Ser
 645 650 655
 Asp Ile Thr Asn Leu Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Asp
 660 665 670
 Val Glu Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln
 675 680 685
 Met Ile Ser Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg
 690 695 700
 Glu Ala Ala Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn
 705 710 715 720
 Met Ser His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr
 725 730 735
 Gln Leu Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu
 740 745 750
 Asn Ile Val Asn Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp
 755 760 765
 Ile Leu Asp Leu Ser Lys Ile Glu Ala Arg Arg Met Val Ile Glu Glu
 770 775 780
 Ile Pro Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu
 785 790 795 800
 Ala Val Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Lys Val Asp
 805 810 815
 Ser Ser Val Pro Asp Tyr Val Ile Gly Asp Ser Phe Arg Leu Arg Gln
 820 825 830

Ile Ile Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly			
835	840	845	
Glu Val Ser Leu Thr Ile Lys Glu Ser Met Gly Gln Asn Asn Val Arg			
850	855	860	
Pro Gly Glu Tyr Ala Val Glu Phe Val Val Glu Asp Thr Gly Ile Gly			
865	870	875	880
Ile Ala Gln Asp Lys Leu Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala			
885	890	895	
Asp Gly Ser Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser			
900	905	910	
Ile Ser Lys Arg Leu Val Asn Leu Met Gly Gly Asp Leu Trp Val Asn			
915	920	925	
Ser Glu His Gly Lys Gly Ser Glu Phe His Phe Thr Cys Leu Val Lys			
930	935	940	
Leu Ala Pro Asp Asp Ala Ala Leu Ile Glu Gln Gln Ile Arg Pro Tyr			
945	950	955	960
Arg Gly His Gln Val Leu Phe Val Asp Lys Ala Gln Ser Gln Asn Ala			
965	970	975	
Thr Ser Ile Lys Pro Met Leu Glu Lys Ile Gly Leu Lys Pro Val Val			
980	985	990	
Val Asp Ser Glu Lys Ser Pro Ala Leu Thr Arg Leu Gln Ser Gly Gly			
995	1000	1005	
Ser Leu Pro Tyr Asp Ala Ile Leu Val Asp Ser Ile Asp Thr Ala Arg			
1010	1015	1020	
Arg Leu Arg Ala Val Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu			
1025	1030	1035	1040

Ala Pro Val Val His Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile			
1045	1050	1055	
Thr Ser Tyr Met Thr Thr Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly			
1060	1065	1070	
Met Ile Pro Ala Leu Glu Asn Arg Ala Thr Pro Ser Leu Ala Asp Asn			
1075	1080	1085	
Thr Lys Ser Phe Glu Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln			
1090	1095	1100	
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val			
1105	1110	1115	1120
Val Gly Asn Gly Trp Glu Ala Val Lys Ala Val Gln Ser Lys Lys Phe			
1125	1130	1135	
Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu			
1140	1145	1150	
Ala Thr Gly Lys Ile Arg Glu Tyr Glu Arg Gly Ile Gly Ser His Arg			
1155	1160	1165	
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Met Gly Asp Arg Glu			
1170	1175	1180	
Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln			
1185	1190	1195	1200
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly			
1205	1210	1215	
Pro Leu Leu Glu Lys Asn Arg Glu Arg Glu Leu Ala Leu His Ala Glu			
1220	1225	1230	
Thr Lys Ser Lys His Lys Glu Gly Gly Gln Gly Leu Leu Arg Pro Thr			
1235	1240	1245	

Leu Glu Ser Arg Ser Phe Thr Ser Arg Glu Pro Leu Leu Gly Asn Gly

1250

1255

1260

Lys Glu Ser Pro Ala Ile Leu Ala Thr Asp Glu Asp Pro Leu Ala Arg

1265

1270

1275

1280

Ala Arg Leu Asp Leu Ser Asp Met Arg Ser Leu Thr Asn

1285

1290

<210> 42

<211> 3882

<212> DNA

<213> *Fusarium oxysporum*

<220>

<221> CDS

<222> (1)..(3882)

<400> 42

atg gtt gac gac gcg gcc ctc gcc gct gcg gct tcg att gtc gcc tcg 48

Met Val Asp Asp Ala Ala Leu Ala Ala Ala Ser Ile Val Ala Ser

1

5

10

15

att gct cca gat ccc cgt ctg ccc aat tcg ata ccg gtt ggt gta gct 96

Ile Ala Pro Asp Pro Arg Leu Pro Asn Ser Ile Pro Val Gly Val Ala

20

25

30

tct cag gtg caa ctc cca ggg cca gat act ccc gcc aag cgc aag ctc	144
Ser Gln Val Gln Leu Pro Gly Pro Asp Thr Pro Ala Lys Arg Lys Leu	
35 40 45	
 gaa ctc gag ctt cag aac ctt gct cta cgt gtt gga aag ctc gag agc	192
Glu Leu Glu Leu Gln Asn Leu Ala Leu Arg Val Gly Lys Leu Glu Ser	
50 55 60	
 cag gcc tca gct acc tct cca ttc cca gaa acg ccc aac gag gtt att	240
Gln Ala Ser Ala Thr Ser Pro Phe Pro Glu Thr Pro Asn Glu Val Ile	
65 70 75 80	
 gac act ctt ttt ggc gaa gag gct cag gct gtg gcg gtc cgt ccc aag	288
Asp Thr Leu Phe Gly Glu Glu Ala Gln Ala Val Ala Val Arg Pro Lys	
85 90 95	
 cct aaa gtc ttt cac gcc caa ggt agc ctg cac tct ccg cat ctg cca	336
Pro Lys Val Phe His Ala Gln Gly Ser Leu His Ser Pro His Leu Pro	
100 105 110	
 tct tat cag ctg acc gaa gaa gcc ctt gaa gga ctt cga gaa cat gtg	384
Ser Tyr Gln Leu Thr Glu Glu Ala Leu Glu Gly Leu Arg Glu His Val	
115 120 125	
 gac gac caa tcc aag tta ctc gat agt cag cgc cag gag ctc gct ggt	432
Asp Asp Gln Ser Lys Leu Leu Asp Ser Gln Arg Gln Glu Leu Ala Gly	

130	135	140	
gta aat gct cag ctc ttg gag cag aag cag cta caa gag cga gcc ctc			480
Val Asn Ala Gln Leu Leu Glu Gln Lys Gln Leu Gln Glu Arg Ala Leu			
145	150	155	160
gag atc ctc gag cag gaa cgt att gct act ctg gag cgc gag ctt tgg			528
Glu Ile Leu Glu Gln Glu Arg Ile Ala Thr Leu Glu Arg Glu Leu Trp			
	165	170	175
aag cat cag aaa gcc aac gag gct ttc caa aag gct cta cga gaa att			576
Lys His Gln Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile			
180	185	190	
gga gag att gtt aca gcc gtt gct cgc ggt gat ttg acc atg aag gtt			624
Gly Glu Ile Val Thr Ala Val Ala Arg Gly Asp Leu Thr Met Lys Val			
195	200	205	
cgc atg aac act gtt gaa atg gac cct gaa atc aca aca ttc aag cgc			672
Arg Met Asn Thr Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg			
210	215	220	
act atc aac gct atg atg gac cag ctg caa ata ttt gct agc gaa gtc			720
Thr Ile Asn Ala Met Met Asp Gln Leu Gln Ile Phe Ala Ser Glu Val			
225	230	235	240

tcg cga gtc gct cgt gaa gtc ggt acc gaa gga ttg ctt ggt ggc caa	768
Ser Arg Val Ala Arg Glu Val Gly Thr Glu Gly Leu Leu Gly Gly Gln	
245 250 255	
gcc cgt atc ggc ggc gtc gac gga aca tgg aag gaa ttg act gac aac	816
Ala Arg Ile Gly Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn	
260 265 270	
gta aac gtt atg gcc cag aat ctt act gat caa gtg agg gag ata gca	864
Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala	
275 280 285	
tcg gtt acc acc gcc gtg gcc cac ggc gat ctg act aaa aag atc gaa	912
Ser Val Thr Thr Ala Val Ala His Gly Asp Leu Thr Lys Lys Ile Glu	
290 295 300	
cga cct gcc aga ggc gag ata ttg caa tta caa caa acg att aac acc	960
Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr	
305 310 315 320	
atg gtg gac caa tta cga aca ttt gct tct gaa gtc aca cgt gta gcg	1008
Met Val Asp Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala	
325 330 335	
aga gat gtc ggg acc gaa ggc atg tta ggc ggg caa gcc gat gtt ggg	1056
Arg Asp Val Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Gly	

340	345	350	
gga gtg cag ggc atg tgg aac gat ctc acc gtc aat gtc aat gcc atg			1104
Gly Val Gln Gly Met Trp Asn Asp Leu Thr Val Asn Val Asn Ala Met			
355	360	365	
gcc aac aac ttg acg act caa gtg cgc gac att atc aag gtt acc aca			1152
Ala Asn Asn Leu Thr Thr Gln Val Arg Asp Ile Ile Lys Val Thr Thr			
370	375	380	
gct gtc gcc aag gga gat ctt aca caa aag gtc caa gcc gat tgc agg			1200
Ala Val Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Asp Cys Arg			
385	390	395	400
gga gag ata ttc gag ctc aag tca acc atc aac tcc atg gtt gac cag			1248
Gly Glu Ile Phe Glu Leu Lys Ser Thr Ile Asn Ser Met Val Asp Gln			
405	410	415	
ctg caa cag ttc gcc cgc gag gtt acc aag att gcc cgt gaa gtc gga			1296
Leu Gln Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly			
420	425	430	
acc gaa gga cgc ctg gga ggg cag gcc act gtg cat gat gtt gaa ggc			1344
Thr Glu Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly			
435	440	445	

acc tgg agg gat ctg acg gag aac gtc aac ggc atg gcc atg aac ttg	1392
Thr Trp Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu	
450 455 460	
acc act caa gtg cga gaa att gcc aag gtt aca aca gct gtc gcc aaa	1440
Thr Thr Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Lys	
465 470 475 480	
ggt gac ttg aca aag aag att ggg gtt gag gtc aag ggt gaa att gca	1488
Gly Asp Leu Thr Lys Lys Ile Gly Val Glu Val Lys Gly Glu Ile Ala	
485 490 495	
gaa ctg aag aac acc att aac cag atg gtg gat cgt ctt ggt acg ttt	1536
Glu Leu Lys Asn Thr Ile Asn Gln Met Val Asp Arg Leu Gly Thr Phe	
500 505 510	
gcc gtt gag gtg agc aag gta gcc agg gaa gta ggc aca gat gga aca	1584
Ala Val Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr	
515 520 525	
ttg ggt gga cag gct caa gtt gcc aat gtt gaa ggt aaa tgg aag gat	1632
Leu Gly Gly Gln Ala Gln Val Ala Asn Val Glu Gly Lys Trp Lys Asp	
530 535 540	
ctc aca gaa aac gtc aac aca atg gcg tca aat ctc aca gtc cag gtc	1680
Leu Thr Glu Asn Val Asn Thr Met Ala Ser Asn Leu Thr Val Gln Val	

545	550	555	560	
cga agt atc tca aca gtt act caa gcc att gcg aac ggc gac atg agc	1728			
Arg Ser Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser				
565	570	575		
cag aag atc aag gtc gaa gca aat gga gag ata caa gtg ctg aaa gaa	1776			
Gln Lys Ile Lys Val Glu Ala Asn Gly Glu Ile Gln Val Leu Lys Glu				
580	585	590		
acc atc aat aac atg gtt gac cgt ttg tct agc ttc tgt tac gaa gtg	1824			
Thr Ile Asn Asn Met Val Asp Arg Leu Ser Ser Phe Cys Tyr Glu Val				
595	600	605		
cag cga gtt gcc aag gat gtg ggt gtt gat gga aag atg ggt gct caa	1872			
Gln Arg Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Ala Gln				
610	615	620		
gcc gac gta ggt ggt cta gac ggc cgc tgg aaa gag atc acc aca gat	1920			
Ala Asp Val Gly Gly Leu Asp Gly Arg Trp Lys Glu Ile Thr Thr Asp				
625	630	635	640	
gtc aac aca atg gct agt aac ctg act aca caa gtg cgc gcc ttc tca	1968			
Val Asn Thr Met Ala Ser Asn Leu Thr Thr Gln Val Arg Ala Phe Ser				
645	650	655		

gat ata acc aac ttg gcc acc gac ggg gat ttc acc aag cta gtc gac	2016
Asp Ile Thr Asn Leu Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Asp	
660 665 670	
gtc gaa gca tcg ggt gag atg gac gag ctc aag cgc aag atc aac cag	2064
Val Glu Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln	
675 680 685	
atg att tca aat ctg cgc gat tct att cag cgt aat act cag gcc agg	2112
Met Ile Ser Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg	
690 695 700	
gaa gct gcc gaa ctt gcc aac aag acc aag tca gag ttc ctc gcc aac	2160
Glu Ala Ala Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn	
705 710 715 720	
atg tcc cat gaa att cga acg ccg atg aac ggt atc atc gga atg act	2208
Met Ser His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr	
725 730 735	
caa ctg aca ttg gac acc gat ctg act caa tat cag agg gag atg ctt	2256
Gln Leu Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu	
740 745 750	
aac att gtc aat aat ctt gcc aat agc ctc ttg acg ata att gac gat	2304
Asn Ile Val Asn Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp	

755

760

765

atc ttg gat ctt tcc aag att gaa gct cgg aga atg gtc att gag gag 2352

Ile Leu Asp Leu Ser Lys Ile Glu Ala Arg Arg Met Val Ile Glu Glu

770

775

780

att cct tac aca ctg cgt gga acc gtc ttc aat gcc ctc aag act ctc 2400

Ile Pro Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu

785

790

795

800

gct gtc aag gca aat gag aag ttc ttg gat ctc acc tac aag gtc gat 2448

Ala Val Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Lys Val Asp

805

810

815

agc tcc gtg cct gac tac gtt att ggc gac tcc ttc cgt ctc aga caa 2496

Ser Ser Val Pro Asp Tyr Val Ile Gly Asp Ser Phe Arg Leu Arg Gln

820

825

830

att atc ctc aac ctt gtt ggc aat gct atc aag ttc aca gag cat ggt 2544

Ile Ile Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly

835

840

845

gag gtc agc cta acg atc aag gag agc atg ggg caa aac aat gtc cga 2592

Glu Val Ser Leu Thr Ile Lys Glu Ser Met Gly Gln Asn Asn Val Arg

850

855

860

cct gga gag tat gcg gtt gag ttt gtc gtg gag gac acg ggc ata gga	2640
Pro Gly Glu Tyr Ala Val Glu Phe Val Val Glu Asp Thr Gly Ile Gly	
865 870 875 880	
atc gcc caa gat aaa ctg gat ttg atc ttc gac acg ttc caa caa gcg	2688
Ile Ala Gln Asp Lys Leu Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala	
885 890 895	
gat ggt tcc atg acg cgc aag ttt ggc gga aca ggt cta ggt cta tct	2736
Asp Gly Ser Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser	
900 905 910	
att tcg aaa cga ctc gtc aat ctc atg ggt ggt gat ctc tgg gta aac	2784
Ile Ser Lys Arg Leu Val Asn Leu Met Gly Gly Asp Leu Trp Val Asn	
915 920 925	
agt gaa cat ggc aag ggc agt gaa ttt cac ttc aca tgc tta gtc aag	2832
Ser Glu His Gly Lys Gly Ser Glu Phe His Phe Thr Cys Leu Val Lys	
930 935 940	
ctt gct cct gac gat gct gct ctg atc gag caa cag atc cgc ccc tac	2880
Leu Ala Pro Asp Asp Ala Ala Leu Ile Glu Gln Gln Ile Arg Pro Tyr	
945 950 955 960	
cga ggt cat caa gtg cta ttc gtc gac aag gcc cag tcg cag aac gcc	2928
Arg Gly His Gln Val Leu Phe Val Asp Lys Ala Gln Ser Gln Asn Ala	

965	970	975	
acc tca atc aag cct atg ctt gag aag atc ggg ctg aag cct gtc gtt			2976
Thr Ser Ile Lys Pro Met Leu Glu Lys Ile Gly Leu Lys Pro Val Val			
980	985	990	
gtg gat tcg gag aag agt cct gcg ctg act cgt ctt caa agc ggt ggc			3024
Val Asp Ser Glu Lys Ser Pro Ala Leu Thr Arg Leu Gln Ser Gly Gly			
995	1000	1005	
tcc ctt ccc tat gat gct atc ctc gtc gat tcc atc gac act gcg aga			3072
Ser Leu Pro Tyr Asp Ala Ile Leu Val Asp Ser Ile Asp Thr Ala Arg			
1010	1015	1020	
agg tta aga gcc gtg gac gat ttc aag tac ctt cct atc gtc ttg ctg			3120
Arg Leu Arg Ala Val Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu			
1025	1030	1035	1040
gca cca gtt gtt cac gtt agt ctg aag tcg tgc ttg gat ctg gga att			3168
Ala Pro Val Val His Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile			
1045	1050	1055	
acg tcg tat atg acc acg cca tgc aag ctc att gat cta gga aat ggc			3216
Thr Ser Tyr Met Thr Thr Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly			
1060	1065	1070	

atg att ccg gct ctc gag aac cgg gcg aca cct tca ctc gct gac aac	3264
Met Ile Pro Ala Leu Glu Asn Arg Ala Thr Pro Ser Leu Ala Asp Asn	
1075 1080 1085	
acg aaa tct ttc gaa att ctg ctc gcc gaa gac aac acc gtc aac caa	3312
Thr Lys Ser Phe Glu Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln	
1090 1095 1100	
cga tta gca gtg aaa att ctc gag aag tat cac cat gtg gta aca gtg	3360
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val	
1105 1110 1115 1120	
gtt ggt aac ggc tgg gaa gct gtc aaa gcc gtc caa agc aag aaa ttc	3408
Val Gly Asn Gly Trp Glu Ala Val Lys Ala Val Gln Ser Lys Lys Phe	
1125 1130 1135	
gat gtc att ctt atg gat gta caa atg ccg atc atg gga ggc ttc gaa	3456
Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu	
1140 1145 1150	
gcc acg ggc aag att cga gaa tac gaa cgt ggc ata ggg agc cac cgc	3504
Ala Thr Gly Lys Ile Arg Glu Tyr Glu Arg Gly Ile Gly Ser His Arg	
1155 1160 1165	
aca ccc atc att gct cta acg gcc cac gcc atg atg ggt gac cga gag	3552
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Met Gly Asp Arg Glu	

1170	1175	1180	
aag tgt atc caa gct cag atg gac gag tat ttg tcc aaa ccc ttg cag			3600
Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln			
1185	1190	1195	1200
caa aac cat ctc atc cag acg atc ctc aaa tgc gcg acg ctc ggc ggc			3648
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly			
1205	1210	1215	
cct ttg ctt gaa aag aat cgt gaa cgg gaa ctg gca ctt cat gcc gag			3696
Pro Leu Leu Glu Lys Asn Arg Glu Arg Glu Leu Ala Leu His Ala Glu			
1220	1225	1230	
acg aaa tcg aag cac aag gag ggg gga cag ggt ctg cta cga ccc aca			3744
Thr Lys Ser Lys His Lys Glu Gly Gly Gln Gly Leu Leu Arg Pro Thr			
1235	1240	1245	
ctc gag agc cgc tca ttc aca agt cga gaa cct ctg ttg gga aat ggc			3792
Leu Glu Ser Arg Ser Phe Thr Ser Arg Glu Pro Leu Leu Gly Asn Gly			
1250	1255	1260	
aag gag agc cct gcc att ctg gct act gat gag gat ccc ctg gca aga			3840
Lys Glu Ser Pro Ala Ile Leu Ala Thr Asp Glu Asp Pro Leu Ala Arg			
1265	1270	1275	1280

gca cgt ctt gac ctc tct gat atg cga agt ctt acc aac taa 3882

Ala Arg Leu Asp Leu Ser Asp Met Arg Ser Leu Thr Asn

1285

1290

<210> 43

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 43

tcagatcgcc gtgggccacg gcggtggta

29

<210> 44

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 44

cgacaaggcc cagtcgcaga acgccacc

28

<210> 45

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 45

aagtttggcg gaacaggtct aggtctatc

29

<210> 46

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 46

tgccagcaag acgataggaa ggtacttga

29

<210> 47

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 47

cctcaccatg ctctgtgaac ttgatagc

28

<210> 48

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 48

gccatttgtg tgacatctgt ggtgatctc

29

<210> 49

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 49

gatgcttcca aagctcgccg tccagagtag

30

<210> 50

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 50

ccgaagacaa caccgtcaac caacgattag

30

<210> 51

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 51

ggaccctgaa atcacaacat tcaagcgc

28

<210> 52

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 52

tgcaactagta tggttgacga cgcggccctc gc

32

<210> 53

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 53

gagctgcagt tagttggtaa gacttcgcat atc

33

<210> 54

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 54

gtaaaacgac ggccag

16

<210> 55

<211> 1307

<212> PRT

<213> *Mycosphaerella tritici*

<400> 55

Met Leu Gln Glu Glu Thr Ser Ala Ala Val Ala Ser Ile Leu Ser Asn
1 5 10 15
Phe Ala Lys Gln Tyr Ala Pro Leu Glu Ala Asp Ser Phe Pro Ala Lys
20 25 30
Ala Ile Ala Asn Gly Ile Lys Asn Thr Lys Ile Ala Leu Pro Gly Asp
35 40 45
Asp Ser Val Glu Lys Arg Thr Leu Glu Arg Glu Leu Thr Ser Leu Ala
50 55 60
Thr Arg Ile Gln Phe Leu Glu Ala Arg Ala Thr Ser Gly Thr Ser Ser
65 70 75 80
Leu Pro Ile Thr Pro Asn Glu Pro Leu Ser Ser Ala Phe Ser Glu Asp
85 90 95
Thr Ser Ser Pro Arg Ser Ala Ala Asn Gln His Arg Gln Arg Ser Ser
100 105 110
Ser Trp Val Asn Asn Leu Leu Ala Lys Ser Glu Gly Glu Pro His Pro

115	120	125
Arg Gln Leu Thr Glu Glu Gln Phe Ser Phe Leu Arg Glu His Ile Asp		
130	135	140
Gln Gln Ala Gln Glu Ile Arg Thr Gln Lys Glu Phe Ile Asp Gly Ile		
145	150	155
Lys Ser Gln Leu Thr His Gln Gln Thr Ala Thr Lys Ala Ala Leu Asp		
165	170	175
Thr Leu Gly Asn Ser Gln Ser Ile Glu Gln Leu Lys Arg Glu Ile Glu		
180	185	190
Lys Asn Ala Gln Ile Asn Ala Thr Tyr Gln Lys Val Leu Arg Glu Ile		
195	200	205
Gly Thr Ile Ile Thr Ala Val Ala Asn Gly Asp Leu Ser Lys Lys Val		
210	215	220
Leu Ile His Ala Thr Glu Lys Asp Pro Glu Ile Ala Arg Phe Lys His		
225	230	235
Thr Ile Asn Lys Met Val Asp Gln Leu Gln Glu Phe Ala Ser Gln Val		
245	250	255
Thr His Leu Ala Lys Glu Val Gly Thr Glu Gly Arg Leu Gly Gly Gln		
260	265	270
Ala Val Val Pro Gly Val Asp Gly Ile Trp Ala Glu Leu Thr Gln Asn		
275	280	285
Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala		
290	295	300
Val Val Thr Thr Ala Val Ala Gln Gly Asp Leu Ser Arg Lys Ile Gln		
305	310	315
Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Ser		

325	330	335
Met Val Gly Gln Leu Arg Thr Phe Ala Thr Glu Val Thr Arg Val Ser		
340	345	350
Arg Asp Val Gly Thr Glu Gly Val Leu Gly Gly Gln Ala Gln Ile Glu		
355	360	365
Gly Val Gln Gly Met Trp Ser Asp Leu Thr Val Asn Val Asn Ala Met		
370	375	380
Ala Asn Asn Leu Thr Ala Gln Val Arg Asp Ile Ala Glu Val Thr Thr		
385	390	395
Ala Val Ala Arg Gly Asp Leu Thr Gln Gln Val Lys Ala Gln Cys Lys		
405	410	415
Gly Glu Ile Leu Ala Leu Lys Thr Thr Ile Asn Ser Met Val His Gln		
420	425	430
Leu Arg Gln Phe Ala His Glu Val Thr Lys Ile Ala Arg Glu Val Gly		
435	440	445
Thr Glu Gly Arg Leu Gly Gly Gln Ala Thr Val His Gly Val Glu Gly		
450	455	460
Thr Trp Lys Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu		
465	470	475
Thr Thr Gln Val Arg Glu Ile Ala Glu Val Thr Thr Ala Val Ala Gln		
485	490	495
Gly Asp Leu Ser Lys Lys Val Glu Ala Glu Val Lys Gly Glu Ile Leu		
500	505	510
Ala Leu Lys Ser Thr Ile Asn Ser Met Val Asp Arg Leu Gly Thr Phe		
515	520	525
Ala Phe Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Glu Gly Val		

530	535	540
Leu Gly Gly Gln Ala Glu Val Ala Asn Val Glu Gly Lys Trp Lys Asp		
545	550	555
Leu Thr Asp Asn Val Asn Thr Met Ala Asn Asn Leu Thr Gly Gln Val		
565	570	575
Arg Ser Ile Ser Asp Val Thr Gln Ala Ile Ala Arg Gly Asp Met Ser		
580	585	590
Gln Arg Ile Lys Val His Ala Gln Gly Glu Ile Gln Thr Leu Lys Asp		
595	600	605
Thr Ile Asn Asp Met Val Thr Arg Leu Asp Ala Trp Ser Leu Ala Val		
610	615	620
Lys Arg Val Ala Arg Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln		
625	630	635
Ala Glu Val Glu Gly Ile Thr Gly Arg Trp Lys Glu Ile Thr Thr Asp		
645	650	655
Val Asn Ile Met Ala Gln Asn Leu Thr Ser Gln Val Arg Ala Phe Ala		
660	665	670
Asp Ile Thr His Ala Ala Met Lys Gly Asp Phe Thr Lys Met Ile Asn		
675	680	685
Val Glu Ala Ser Gly Glu Met Asn Glu Leu Lys Asn Lys Ile Asn Lys		
690	695	700
Met Val Leu Asn Leu Arg Glu Ser Ile Gln Lys Asn Asn Gln Ala Arg		
705	710	715
Glu Ala Ala Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn		
725	730	735
Met Ser His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr		

740	745	750
Gln Leu Thr Leu Asp Thr Glu Leu Glu Gln Asn Gln Arg Asp Met Leu		
755	760	765
Asn Ile Val Phe Ser Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp		
770	775	780
Ile Leu Asp Ile Ser Lys Ile Glu Ala Asn Arg Met Ile Leu Glu Glu		
785	790	795
Glu Pro Phe Ser Leu Arg Gly Leu Val Phe Asn Ser Leu Lys Ser Leu		
805	810	815
Ala Val Arg Ala Asn Glu Lys Asp Ile Ser Leu Val Tyr Asp Thr Asp		
820	825	830
Ser Ser Val Pro Asp Tyr Ile Val Gly Asp Ser Phe Arg Leu Arg Gln		
835	840	845
Ile Ile Leu Asn Leu Ala Gly Asn Ala Ile Lys Phe Thr Glu His Gly		
850	855	860
Glu Val Arg Val Lys Ile Phe Ser Asp His Ser Thr Arg Cys Thr Asp		
865	870	875
Ser Glu Val Val Val Lys Phe Ala Val Ser Asp Thr Gly Ile Gly Ile		
885	890	895
His Ser Asn Lys Leu Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp		
900	905	910
Gly Ser Thr Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile		
915	920	925
Ser Arg Arg Leu Val Thr Leu Met Arg Gly Lys Met Trp Val Glu Ser		
930	935	940
Asn Tyr Gly Ser Gly Ser Thr Phe Phe Phe Thr Xaa Val Val Arg Leu		

945	950	955	960
Gly Asn Pro Asp Val Ala Lys Ile Met Pro Gln Leu Gln Gln Tyr Arg			
965	970	975	
Lys His Asn Val Leu Phe Val Asp Asn Gly Asn Thr Asp Ser Ser Glu			
980	985	990	
Glu Ile Ala Ala Gly Ile Arg Ala Leu Asp Leu Val Pro Cys Val Val			
995	1000	1005	
Gly Lys Gly Lys Val Pro His Ser Glu Ile Ser Pro Asp Asp Gln Tyr			
1010	1015	1020	
Asp Cys Val Ile Ile Asp Asn Ser Glu Thr Ala Gln Lys Leu Arg Ser			
1025	1030	1035	1040
Leu Glu Arg Phe Lys Tyr Ile Pro Ile Val Met Val Ala Pro Ala Ile			
1045	1050	1055	
Ser Val Asn Phe Lys Thr Ala Leu Glu Asn Gly Ile Ser Ser Tyr Met			
1060	1065	1070	
Thr Thr Pro Cys Leu Pro Ile Asp Leu Gly Asn Ala Leu Val Pro Ala			
1075	1080	1085	
Leu Glu Gly Arg Ala Ala Pro Met Ser Ala Asp His Ser Arg Thr Phe			
1090	1095	1100	
Asp Ile Leu Leu Ala Glu Asp Asn Ala Val Asn Gln Lys Leu Ala Val			
1105	1110	1115	1120
Lys Ile Leu Thr Lys His Asn His Thr Val Thr Val Ala Asn Asn Gly			
1125	1130	1135	
Leu Glu Ala Phe Glu Ala Ile Arg Lys Lys Arg Phe Asp Val Val Leu			
1140	1145	1150	
Met Asp Val Gln Met Pro Val Met Gly Gly Phe Glu Ala Thr Ala Lys			

1155	1160	1165
Ile Arg Glu Tyr Glu Arg Thr His Glu Leu Ala Arg Ser Pro Ile Ile		
1170	1175	1180
Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu Lys Cys Ile Gln		
1185	1190	1195
Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys Xaa Asn Gln Leu		
1205	1210	1215
Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly Ala Leu Leu Asp		
1220	1225	1230
Arg Arg Asn Asp Gly Arg Gly Leu Leu Met Glu Glu Asp Lys Pro Val		
1235	1240	1245
Ser Asp Asn Ser Ser Leu Pro Ala Asp His Asn Arg Leu Leu Thr Pro		
1250	1255	1260
Pro Lys Arg Pro Gly Val Asp Arg Gly Tyr Thr Glu Asn Gly Pro Pro		
1265	1270	1275
Gly Leu Glu Ser Pro Ala Ile Val Thr Asp Asp Gln Asp Asp Pro Met		
1285	1290	1295
Ile Arg Glu Ser Leu Val Arg Ala His Ser Ser		
1300	1305	

<210> 56

<211> 3924

<212> DNA

<213> *Mycosphaella tritici*

<220>

<221> CDS

<222> (1).. (3924)

<400> 56

atg ctg caa gaa gag act tcg gca gct gtg gcc agc atc ctc tcc aac 48

Met Leu Gln Glu Glu Thr Ser Ala Ala Val Ala Ser Ile Leu Ser Asn

1 5 10 15

ttc gcc aag cag tat gct cct ctg gaa gcg gat tca ttc cct gca aag 96

Phe Ala Lys Gln Tyr Ala Pro Leu Glu Ala Asp Ser Phe Pro Ala Lys

20 25 30

gcc atc gcg aat gga att aag aac acc aaa att gct cta ccg ggc gat 144

Ala Ile Ala Asn Gly Ile Lys Asn Thr Lys Ile Ala Leu Pro Gly Asp

35 40 45

gat tca gtg gag aag cgt act cta gag cgc gag ctg act agc ctt gcg 192

Asp Ser Val Glu Lys Arg Thr Leu Glu Arg Glu Leu Thr Ser Leu Ala

50 55 60

acg cgg atc cag ttt ctc gag gct cgc gct aca agc gga acc agt tcg 240

Thr Arg Ile Gln Phe Leu Glu Ala Arg Ala Thr Ser Gly Thr Ser Ser

65 70 75 80

tta ccc atc act ccc aac gag cca ctt tct tcg gca ttc tcg gag gac 288

Leu Pro Ile Thr Pro Asn Glu Pro Leu Ser Ser Ala Phe Ser Glu Asp	
85 90 95	
acc tcg tcg cca agg tcc gca gcg aac cag cac cgc cag cgc tca tcg	336
Thr Ser Ser Pro Arg Ser Ala Ala Asn Gln His Arg Gln Arg Ser Ser	
100 105 110	
tca tgg gtc aac aac ctc ctg gct aag agc gag ggc gag cct cat cct	384
Ser Trp Val Asn Asn Leu Leu Ala Lys Ser Glu Gly Glu Pro His Pro	
115 120 125	
cga caa ctc act gaa gaa caa ttt tca ttt cta cgt gag cac atc gac	432
Arg Gln Leu Thr Glu Glu Gln Phe Ser Phe Leu Arg Glu His Ile Asp	
130 135 140	
caa caa gcg caa gag att cgg act cag aag gaa ttt atc gac ggt atc	480
Gln Gln Ala Gln Glu Ile Arg Thr Gln Lys Glu Phe Ile Asp Gly Ile	
145 150 155 160	
aaa tcg cag ctg acg cac cag caa acc gct aca aaa gct gca ctc gat	528
Lys Ser Gln Leu Thr His Gln Gln Thr Ala Thr Lys Ala Ala Leu Asp	
165 170 175	
acc ttg ggc aac tcg cag tca atc gag cag ctg aag cgg gag att gag	576
Thr Leu Gly Asn Ser Gln Ser Ile Glu Gln Leu Lys Arg Glu Ile Glu	
180 185 190	

aaa aat gcg caa atc aat gct aca tac caa aaa gtg ctg cga gag atc	624
Lys Asn Ala Gln Ile Asn Ala Thr Tyr Gln Lys Val Leu Arg Glu Ile	
195 200 205	
ggc acc atc att aca gct gtc gcc aat gga gat ctc agc aag aaa gtg	672
Gly Thr Ile Ile Thr Ala Val Ala Asn Gly Asp Leu Ser Lys Lys Val	
210 215 220	
ctc att cat gcc acg gag aaa gat ccg gag att gcg agg ttc aag cac	720
Leu Ile His Ala Thr Glu Lys Asp Pro Glu Ile Ala Arg Phe Lys His	
225 230 235 240	
acg atc aac aag atg gtg gac cag ttg caa gag ttt gct agt caa gta	768
Thr Ile Asn Lys Met Val Asp Gln Leu Gln Glu Phe Ala Ser Gln Val	
245 250 255	
aca cat ttg gcg aaa gag gtg gga aca gaa gga cgc ctc gga gga caa	816
Thr His Leu Ala Lys Glu Val Gly Thr Glu Gly Arg Leu Gly Gly Gln	
260 265 270	
gcc gtc gtg cct ggc gtc gac ggt att tgg gcg gag ctt acg caa aac	864
Ala Val Val Pro Gly Val Asp Gly Ile Trp Ala Glu Leu Thr Gln Asn	
275 280 285	
gtg aac gtc atg gcc caa aat ttg acc gac cag gtg cga gaa atc gca	912

Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala	
290	300
gtt gta acc acc gcc gtt gca caa ggt gat ctg agc cgc aag att caa	960
Val Val Thr Thr Ala Val Ala Gln Gly Asp Leu Ser Arg Lys Ile Gln	
305	320
cga cca gcc aga ggc gag att ctc caa ctt caa cag act atc aac tcc	1008
Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Ser	
325	335
atg gtg gga cag ctc cgg acc ttc gca acg gaa gtt acg aga gtg tcg	1056
Met Val Gly Gln Leu Arg Thr Phe Ala Thr Glu Val Thr Arg Val Ser	
340	350
cgc gat gtc ggc acg gag ggt gtt ctt gga ggt caa gct caa atc gaa	1104
Arg Asp Val Gly Thr Glu Gly Val Leu Gly Gly Gln Ala Gln Ile Glu	
355	365
ggc gta cag ggc atg tgg agc gac ctt act gtg aac gtg aat gct atg	1152
Gly Val Gln Gly Met Trp Ser Asp Leu Thr Val Asn Val Asn Ala Met	
370	380
gca aac aat ctc act gcc cag gtg cga gat att gcg gag gtg aca aca	1200
Ala Asn Asn Leu Thr Ala Gln Val Arg Asp Ile Ala Glu Val Thr Thr	
385	400

gcc gtg gcc cga ggc gac ctc acg cag cag gtt aaa gcg caa tgt aag	1248
Ala Val Ala Arg Gly Asp Leu Thr Gln Gln Val Lys Ala Gln Cys Lys	
405 410 415	
ggg gag atc ctg gcc ttg aaa acc acc atc aac tcc atg gtg cac cag	1296
Gly Glu Ile Leu Ala Leu Lys Thr Thr Ile Asn Ser Met Val His Gln	
420 425 430	
cta cgg caa ttc gcg cat gaa gtc acc aag atc gcg cgt gag gtc ggg	1344
Leu Arg Gln Phe Ala His Glu Val Thr Lys Ile Ala Arg Glu Val Gly	
435 440 445	
aca gaa ggt cgc cta ggt gga caa gca aca gtt cac gga gtc gag ggc	1392
Thr Glu Gly Arg Leu Gly Gly Gln Ala Thr Val His Gly Val Glu Gly	
450 455 460	
aca tgg aaa gac ttg acg gag aac gta aat ggc atg gcc atg aat ctg	1440
Thr Trp Lys Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu	
465 470 475 480	
acc acc caa gtg cgc gag atc gca gaa gtc aca acc gcc gtc gcg caa	1488
Thr Thr Gln Val Arg Glu Ile Ala Glu Val Thr Thr Ala Val Ala Gln	
485 490 495	
gga gat ctc agc aaa aag gtc gag gcc gaa gtc aag ggt gaa att ttg	1536

Gly Asp Leu Ser Lys Lys Val Glu Ala Glu Val Lys Gly Glu Ile Leu

500

505

510

gcc ttg aag agc acc atc aat tcc atg gtt gac cgt ctg ggt acg ttt 1584

Ala Leu Lys Ser Thr Ile Asn Ser Met Val Asp Arg Leu Gly Thr Phe

515

520

525

gct ttc gag gtt agc aag gtc gcg aga gaa gtc gga acc gaa gga gtt 1632

Ala Phe Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Glu Gly Val

530

535

540

ttg ggc gga caa gca gag gtt gcc aat gtc gaa gga aaa tgg aaa gat 1680

Leu Gly Gly Gln Ala Glu Val Ala Asn Val Glu Gly Lys Trp Lys Asp

545

550

555

560

ctt acc gac aat gtc aac acc atg gcc aac aac ttg act ggt cag gtg 1728

Leu Thr Asp Asn Val Asn Thr Met Ala Asn Asn Leu Thr Gly Gln Val

565

570

575

cgg agc att tca gac gtc aca cag gcc att gca cgc ggt gac atg agc 1776

Arg Ser Ile Ser Asp Val Thr Gln Ala Ile Ala Arg Gly Asp Met Ser

580

585

590

cag cga atc aag gtg cac gct cag gga gag att cag aca ttg aag gac 1824

Gln Arg Ile Lys Val His Ala Gln Gly Glu Ile Gln Thr Leu Lys Asp

595

600

605

acg atc aac gac atg gtg acg cga ctg gac gct tgg tca ctc gcg gtg	1872
Thr Ile Asn Asp Met Val Thr Arg Leu Asp Ala Trp Ser Leu Ala Val	
610 615 620	
aag cgg gtg gct cgt gac gtc ggt gtc gac ggc aag atg ggt gga cag	1920
Lys Arg Val Ala Arg Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln	
625 630 635 640	
gca gaa gtc gaa ggc atc act ggt cgc tgg aag gag atc acg acc gat	1968
Ala Glu Val Glu Gly Ile Thr Gly Arg Trp Lys Glu Ile Thr Thr Asp	
645 650 655	
gtg aac att atg gct caa aat ttg acc tcg caa gtg aga gct ttt gcc	2016
Val Asn Ile Met Ala Gln Asn Leu Thr Ser Gln Val Arg Ala Phe Ala	
660 665 670	
gac att acc cac gcg gcc atg aaa gga gat ttc acc aag atg atc aat	2064
Asp Ile Thr His Ala Ala Met Lys Gly Asp Phe Thr Lys Met Ile Asn	
675 680 685	
gtc gaa gcg tct ggc gaa atg aac gag ctg aag aac aag atc aac aag	2112
Val Glu Ala Ser Gly Glu Met Asn Glu Leu Lys Asn Lys Ile Asn Lys	
690 695 700	
atg gtc ctc aac ttg cgc gaa agt atc cag aag aac aat caa gca aga	2160

Met Val Leu Asn Leu Arg Glu Ser Ile Gln Lys Asn Asn Gln Ala Arg

705 710 715 720

gag gcc gcc gag ttg gcc aac aag acg aaa tcg gag ttc ctg gca aac 2208

Glu Ala Ala Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn

725 730 735

atg tcc cac gag att cga aca cct atg aac gga atc atc gga atg aca 2256

Met Ser His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr

740 745 750

cag ctt acc ttg gac acc gag ctt gag cag aac caa cgg gac atg ctc 2304

Gln Leu Thr Leu Asp Thr Glu Leu Glu Gln Asn Gln Arg Asp Met Leu

755 760 765

aac atc gtc ttc tcg ctc gcc aac agc tta ctg acg att att gat gac 2352

Asn Ile Val Phe Ser Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp

770 775 780

atc ttg gac att tcc aag att gaa gca aat cgc atg atc cta gag gaa 2400

Ile Leu Asp Ile Ser Lys Ile Glu Ala Asn Arg Met Ile Leu Glu Glu

785 790 795 800

gag ccg ttc tca ctg cga ggt ctc gtc ttc aac agc tta aag tca ctt 2448

Glu Pro Phe Ser Leu Arg Gly Leu Val Phe Asn Ser Leu Lys Ser Leu

805 810 815

gca gtc cga gcc aac gag aag gac atc agc ttg gtg tat gat acc gac	2496
Ala Val Arg Ala Asn Glu Lys Asp Ile Ser Leu Val Tyr Asp Thr Asp	
820 825 830	
agc tca gtg ccc gac tac atc gtg ggc gac tcc ttc cga ctt cga cag	2544
Ser Ser Val Pro Asp Tyr Ile Val Gly Asp Ser Phe Arg Leu Arg Gln	
835 840 845	
atc att ctc aat ctc gcc ggc aac gcc atc aaa ttc acc gag cac ggg	2592
Ile Ile Leu Asn Leu Ala Gly Asn Ala Ile Lys Phe Thr Glu His Gly	
850 855 860	
gaa gtg cgt gtt aag ata ttc tct gac cac agt aca cga tgc acc gat	2640
Glu Val Arg Val Lys Ile Phe Ser Asp His Ser Thr Arg Cys Thr Asp	
865 870 875 880	
agt gag gtt gtc gtc aaa ttc gcc gtc tcc gat act ggt att ggc atc	2688
Ser Glu Val Val Val Lys Phe Ala Val Ser Asp Thr Gly Ile Gly Ile	
885 890 895	
cac tcc aac aag ttg gat ttg atc ttc gac acg ttt cag cag gct gac	2736
His Ser Asn Lys Leu Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp	
900 905 910	
ggg tcg acc aca cgg aag ttc gga ggt act gga ttg ggc ctg tcg atc	2784

Gly Ser Thr Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile	
915	920
tct cgg aga ctg gtg act ttg atg cgt ggc aag atg tgg gtc gaa tca	2832
Ser Arg Arg Leu Val Thr Leu Met Arg Gly Lys Met Trp Val Glu Ser	
930	935
aat tat ggc tca ggc agc aca ttc ttc ttc acc tgc gtt gta cgg ctg	2880
Asn Tyr Gly Ser Gly Ser Thr Phe Phe Phe Thr Xaa Val Val Arg Leu	
945	950
ggc aat ccg gat gtt gca aaa atc atg cca caa cta cag cag tat cga	2928
Gly Asn Pro Asp Val Ala Lys Ile Met Pro Gln Leu Gln Gln Tyr Arg	
965	970
aag cac aac gtg ctc ttt gtc gac aac ggt aat acg gac agt tcg gag	2976
Lys His Asn Val Leu Phe Val Asp Asn Gly Asn Thr Asp Ser Ser Glu	
980	985
gag atc gcg gct ggc atc cga gct ttg gat ctg gtc cct tgt gtg gtg	3024
Glu Ile Ala Ala Gly Ile Arg Ala Leu Asp Leu Val Pro Cys Val Val	
995	1000
ggc aag gga aag gtt cct cac tcc gaa atc agc cca gac gac cag tac	3072
Gly Lys Gly Lys Val Pro His Ser Glu Ile Ser Pro Asp Asp Gln Tyr	

1010	1015	1020	
gac tgc gtg atc atc gat aac agc gag acg gct cag aag ttg cgc agc			3120
Asp Cys Val Ile Ile Asp Asn Ser Glu Thr Ala Gln Lys Leu Arg Ser			
1025	1030	1035	1040
ttg gaa cgt ttc aag tac att ccc atc gtc atg gtg gcg ccg gcc atc			3168
Leu Glu Arg Phe Lys Tyr Ile Pro Ile Val Met Val Ala Pro Ala Ile			
	1045	1050	1055
tcg gtg aac ttc aag acc gcg ttg gag aac gga atc tca agc tac atg			3216
Ser Val Asn Phe Lys Thr Ala Leu Glu Asn Gly Ile Ser Ser Tyr Met			
1060	1065	1070	
act acg cca tgc ctt cca atc gac ctg ggc aat gct ctg gtg ccc gca			3264
Thr Thr Pro Cys Leu Pro Ile Asp Leu Gly Asn Ala Leu Val Pro Ala			
1075	1080	1085	
ctc gag ggc cgc gca gca ccc atg tca gcc gac cac agt cgg aca ttc			3312
Leu Glu Gly Arg Ala Ala Pro Met Ser Ala Asp His Ser Arg Thr Phe			
1090	1095	1100	
gat atc ctc ctc gca gaa gac aac gcg gtg aat caa aaa ctc gcc gtc			3360
Asp Ile Leu Leu Ala Glu Asp Asn Ala Val Asn Gln Lys Leu Ala Val			
1105	1110	1115	1120

aag atc ctg acc aag cac aac cac aca gtg aca gtc gcc aac aac ggc	3408
Lys Ile Leu Thr Lys His Asn His Thr Val Thr Val Ala Asn Asn Gly	
1125 1130 1135	
ctt gaa gcc ttt gaa gcg att cgc aag aag cgc ttc gat gtc gtt ctc	3456
Leu Glu Ala Phe Glu Ala Ile Arg Lys Lys Arg Phe Asp Val Val Leu	
1140 1145 1150	
atg gac gtg caa atg ccc gtc atg gga ggg ttc gaa gcg acg gcc aag	3504
Met Asp Val Gln Met Pro Val Met Gly Gly Phe Glu Ala Thr Ala Lys	
1155 1160 1165	
att cgc gaa tac gaa cga act cac gag cta gca cgt tcg ccc att atc	3552
Ile Arg Glu Tyr Glu Arg Thr His Glu Leu Ala Arg Ser Pro Ile Ile	
1170 1175 1180	
gcc ctc acc gca cac gcc atg ctt ggc gac cgc gag aag tgt atc caa	3600
Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu Lys Cys Ile Gln	
1185 1190 1195 1200	
gcg caa atg gac gag tat ctc tcc aaa ccc ctc aag ycc aat cag ctc	3648
Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys Xaa Asn Gln Leu	
1205 1210 1215	
att cag acg atc ctg aaa tgt gcg acc cta ggc ggt gcg tta ctt gac	3696
Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly Ala Leu Leu Asp	

1220	1225	1230	
cgg agg aac gat ggg cgc ggt ttg ctc atg gaa gag gac aaa ccc gtt 3744			
Arg Arg Asn Asp Gly Arg Gly Leu Leu Met Glu Glu Asp Lys Pro Val			

1235	1240	1245	
tct gat aat tcg agt ctt cct gca gat cac aat cgg ttg ctc acg ccc 3792			
Ser Asp Asn Ser Ser Leu Pro Ala Asp His Asn Arg Leu Leu Thr Pro			

1250	1255	1260	
ccg aaa cga ccg ggt gtc gat cgt ggg tac acg gag aat gga ccg ccc 3840			
Pro Lys Arg Pro Gly Val Asp Arg Gly Tyr Thr Glu Asn Gly Pro Pro			

1265	1270	1275	1280
ggt ttg gaa agt ccg gcg ata gta acc gac gac cag gat gat ccg atg 3888			
Gly Leu Glu Ser Pro Ala Ile Val Thr Asp Asp Gln Asp Asp Pro Met			

1285	1290	1295	
atc aga gag agt ctt gtt cgt gcc cat agc agc tga 3924			
Ile Arg Glu Ser Leu Val Arg Ala His Ser Ser			

1300	1305
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<210> 57
 <211> 28
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 57

cggaaggagt cgcccacgat gtagtcgg

28

<210> 58

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 58

catggtggcg ccggccatct cggtgaac

28

<210> 59

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 59

tcgccagacg cttcgacatt gatcatcttg

30

<210> 60

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 60

ttcatggcca tgccatttac gttctcgcgc

30

<210> 61

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 61

tacaagcgga accagttcgt taccatcac

30

<210> 62

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 62

gactccttc gacttcgaca gatcattctc

30

<210> 63

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 63

tccgtgtggt cgacccgtca gcctgctg

28

<210> 64

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 64

cccactagta tgctgcaaga agagacttcg

30

<210> 65

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 65

cctaagcttc tcagctgcta tgggcacgaa

30

<210> 66

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 66

caggaaacag ctatgaccat gattacgcca

30

<210> 67

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for DNA sequencing

<400> 67

tgtaaaacga cggccagtga attgtaatac

30

<210> 68

<211> 1438

<212> PRT

<213> Thanatephorus cucumeris

<400> 68

Met	Ala	Gly	Thr	Thr	Gly	Gly	His	Pro	Phe	Thr	Ala	His	Leu	Val	Ala
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Val	Leu	Ser	Ile	Tyr	Glu	Leu	Gly	Pro	Gly	Arg	Pro	Val	Arg	Ala	Leu
			20					25					30		
Pro	Thr	Arg	Ser	Ser	His	Ser	His	Ser	Ser	Ser	Gly	Ser	Arg	His	Ala
			35					40					45		
Arg	Ala	Leu	Ser	Val	Pro	Pro	Phe	Pro	Pro	Pro	Pro	Pro	Met	Ser	Pro
			50					55					60		
Pro	Asn	Ala	Pro	Ile	Asp	Tyr	Val	Gly	Ala	Ala	Pro	Leu	Pro	Arg	Tyr
65							70						75		80

Asp Gly Pro Arg Asp Trp Gln Thr Asp Ala Val Glu Arg Ala Leu Gly			
	85	90	95
Arg Val Ala Ala Arg Met Tyr Ala Ala Glu Ala Gln Leu Gln Asp Leu			
	100	105	110
Leu Ser Arg Glu Ser Ser Thr Ser Thr Pro Asp Pro Ala Leu Ser Pro			
	115	120	125
Arg Ser Asn Gly Leu Lys Lys Arg Arg Glu Asn Pro Gly Thr Pro Asp			
	130	135	140
Glu Arg Asp Pro Trp Gln Thr Val Arg Phe Gln Glu Val Gly Asp Gln			
	145	150	155
Asp Met Asp Pro Glu Pro Asp Thr Pro Val Ala Arg Pro Lys Asp Lys			
	165	170	175
Val Lys Pro Gly Thr Ile Asp Leu Ser Thr Leu Ser Gln Pro Thr Pro			
	180	185	190
Leu Ser Lys Val Ala Thr Asp Asn Pro Val Leu Pro Lys Pro Gly Pro			
	195	200	205
Arg Ser Ala Pro Thr Ser Ser Val Gly Ser Ile Met Pro Pro Phe Thr			
	210	215	220
Cys His Ser Cys Gly Arg Pro Met Gln Gly Pro Ala Ala Pro Asp Val			
	225	230	235
Ile His Ala Pro Gly Pro Leu Asp Val Val Thr Pro Ala Leu Gly Met			
	245	250	255
Gly Leu Gly Leu Ser Asp His Gly Ala Ala Glu Leu Arg Gln Lys Leu			
	260	265	270
Gly Phe Gly Asp His Glu Asp Asp Thr Gly Ser Pro Leu Val Leu Pro			
	275	280	285

Pro Gly Pro Leu Ser Ala Ala Ala Phe Glu Ser Ala Pro Gly Met Ser			
290	295	300	
Ala Val Glu Glu Leu Lys Leu Leu Lys Ala Gln Val Gln Asp Val Ala			
305	310	315	320
Arg Val Cys Lys Ala Val Ala Glu Gly Asp Leu Ser Gln Lys Ile Thr			
325	330	335	
Val Pro Val Gln Gly Pro Val Met Val Gln Leu Lys Asp Val Ile Asn			
340	345	350	
Thr Met Val Asp Lys Leu Gly Arg Phe Ala Gln Glu Val Thr Arg Val			
355	360	365	
Ser Leu Glu Val Gly Thr Glu Gly Arg Leu Gly Gly Gln Ala Ile Val			
370	375	380	
Arg Asp Val Arg Gly Thr Trp Ser Glu Leu Thr Thr Val Val Asn Arg			
385	390	395	400
Leu Ala Ala Asn Leu Thr Ser Gln Val Arg Gly Ile Ala Glu Val Thr			
405	410	415	
Lys Ala Val Ala Lys Gly Asp Leu Ser Lys Gln Ile Gly Val Asp Ala			
420	425	430	
Lys Gly Glu Ile Leu Glu Leu Lys Asn Thr Val Asn Thr Met Val Val			
435	440	445	
Arg Leu Arg Met Phe Ala Gly Glu Val Thr Arg Val Ala Leu Asp Val			
450	455	460	
Gly Ser Arg Gly Ile Leu Gly Gly Gln Ala Tyr Val Pro Asp Val Glu			
465	470	475	480
Gly Val Trp Gln Glu Leu Thr Asp Asn Val Asn Arg Met Cys Ser Asn			
485	490	495	

Leu Thr Asn Gln Val Arg Ser Ile Ala Leu Val Thr Thr Ala Val Ala
 500 505 510
 Glu Gly Asp Leu Thr Arg Lys Ile Glu Ile Glu Val Glu Gly Glu Met
 515 520 525
 Leu Thr Leu Lys Asn Thr Val Asn Ser Met Val Asp Gln Leu Ser Thr
 530 535 540
 Phe Ala Ser Glu Val Thr Arg Val Ala Leu Glu Val Gly Ser Met Gly
 545 550 555 560
 Ile Leu Gly Gly Gln Ala Gln Val Glu Gly Val Lys Gly Thr Trp Ala
 565 570 575
 Asp Leu Thr Arg Asn Val Asn Asn Met Ala Ser Asn Leu Thr Asn Gln
 580 585 590
 Val Arg Ser Ile Ala Lys Val Thr Thr Ala Val Ala His Gly Asp Leu
 595 600 605
 Arg Gln Phe Val Glu Val Asp Val Gln Gly Glu Met Leu Met Leu Lys
 610 615 620
 Asn Thr Val Asn Ser Met Val Ala Gln Leu Asp Thr Leu Ala Ser Glu
 625 630 635 640
 Val Ser Arg Val Ala Leu Glu Val Gly Ile Glu Gly Arg Leu Gly Gly
 645 650 655
 Gln Ala Val Val Gln Gly Val Glu Gly Val Trp Lys Val Leu Thr Asp
 660 665 670
 Asn Val Asn Leu Met Ala Leu Asn Leu Thr Thr Gln Val Arg Ser Ile
 675 680 685
 Ala Ala Val Thr Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Asn Ile
 690 695 700

Asp Val Asp Val Lys Gly Glu Ile Leu Asp Leu Lys Ile Thr Val Asn			
705	710	715	720
Arg Met Thr Asp Ser Leu Arg Ile Phe Ala Ala Glu Val Thr Arg Val			
	725	730	735
Ala Arg Glu Val Gly Thr Leu Gly Arg Leu Gly Gly Gln Ala Phe Val			
	740	745	750
Pro Gly Val Ala Gly Val Trp Lys Asp Leu Thr Asp Asn Val Asn Val			
	755	760	765
Met Ala Ala Asn Leu Thr Leu Gln Val Arg Ala Ile Ala Arg Val Thr			
	770	775	780
Thr Ala Val Ser Val Gly Asp Leu Thr Thr Lys Val Glu Gly Ile Asp			
785	790	795	800
Val Ala Gly Glu Ile Leu Asp Leu Val Asn Thr Ile Asn Gly Met Val			
	805	810	815
Asp Gln Leu Ala Val Phe Ala Ala Glu Val Thr Arg Val Ala Arg Glu			
	820	825	830
Val Gly Thr Glu Gly Arg Leu Gly Val Gln Ala Arg Val Glu Gly Met			
	835	840	845
Gln Gly Ser Trp Gln Ala Ile Thr Val Ser Val Asn Thr Met Ala Ala			
	850	855	860
Asn Leu Thr Ser Gln Val Arg Gly Phe Ala Gln Ile Ser Ala Ala Ala			
865	870	875	880
Thr Asp Gly Asp Phe Thr Arg Phe Ile Thr Val Glu Ala Ser Gly Glu			
	885	890	895
Met Asp Ser Leu Lys Thr Gln Ile Asn Gln Met Val Tyr Asn Leu Arg			
	900	905	910

Glu Ser Ile Gln Arg Asn Thr Ala Ala Arg Glu Ala Ala Glu Leu Ala			
915	920	925	
Asn Arg Ser Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Ile Arg			
930	935	940	
Thr Pro Met Asn Gly Ile Ile Gly Met Thr Asp Leu Thr Leu Asp Thr			
945	950	955	960
Glu Leu Thr Arg Thr Gln Lys Glu Asn Leu Leu Leu Val His Gln Leu			
965	970	975	
Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu Asp Ile Ser Lys			
980	985	990	
Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr Tyr Ser Leu Arg			
995	1000	1005	
Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val Arg Ala His Gln			
1010	1015	1020	
Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu Ile Pro Asp Gln			
1025	1030	1035	1040
Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile Thr Asn Leu Val			
1045	1050	1055	
Gly Asn Ala Ile Lys Phe Thr Pro Ser Lys Pro Asn Lys Lys Gly Met			
1060	1065	1070	
Val Cys Leu Ser Cys Lys Leu Ile Ser Met Asp Glu Gln Asn Val Thr			
1075	1080	1085	
Val Arg Phe Cys Val Glu Asp Thr Gly Ile Gly Ile Lys Gln Asp Lys			
1090	1095	1100	
Leu Ala Ile Ile Phe Asp Thr Phe Cys Gln Ala Asp Gly Ser Thr Thr			
1105	1110	1115	1120

Arg Glu Tyr Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg Leu			
1125	1130	1135	
Val Ser Leu Met Asn Gly Gln Met Trp Val Glu Ser Glu Val Gly Val			
1140	1145	1150	
Gly Ser Arg Phe Tyr Phe Thr Ile Thr Ala Glu Ile Ser Arg Pro Asn			
1155	1160	1165	
Met Ala Gln Ser Leu Gln Lys Val Ala Ile Tyr Lys Glu Arg Thr Ile			
1170	1175	1180	
Leu Phe Val Asp Thr Leu Gly Asp Arg Ser Gly Val Ala Glu Arg Ile			
1185	1190	1195	1200
Glu Glu Leu Gln Leu Arg Pro Phe Val Val Arg Asp Ile Ser Gln Val			
1205	1210	1215	
Ala Asp Lys Ala Lys Ile Pro Phe Ile Asp Thr Val Ile Val Asp Ser			
1220	1225	1230	
Leu Glu Val Thr Glu Lys Leu Arg Glu Leu Asp His Leu Arg Tyr Thr			
1235	1240	1245	
Pro Ala Val Leu Leu Thr Pro Val Met Pro Arg Leu Asn Leu Thr Trp			
1250	1255	1260	
Cys Leu Glu Asn Phe Ile Ser Gly His Val Ala Thr Pro Ser Ser Leu			
1265	1270	1275	1280
Asp Asp Leu Ala Glu Ala Leu Ala Lys Gly Leu Glu Ala Asn Ala Ser			
1285	1290	1295	
Gln Pro Glu Val Thr Pro Ser Asp Val Ala Tyr Asp Ile Leu Leu Ala			
1300	1305	1310	
Glu Asp Asn Val Val Asn Gln Arg Val Ala Val Lys Ile Leu Glu Lys			
1315	1320	1325	

Phe Gly His Thr Val Gln Ile Ala Glu Asn Gly Gln Phe Ala Val Asp			
1330	1335	1340	
Ala Val Lys Ala Arg Tyr Glu Gln Glu Lys Met Phe Asp Val Ile Leu			
1345	1350	1355	1360
Met Asp Val Ser Met Pro Phe Met Gly Gly Met Glu Ala Thr Glu Ile			
	1365	1370	1375
Ile Arg Ala Phe Glu Lys Glu Lys Gly Ile Arg Arg Thr Pro Ile Ile			
	1380	1385	1390
Ala Leu Thr Ala His Ala Met Ile Gly Asp Arg Glu Arg Cys Ile Gln			
	1395	1400	1405
Ala Gly Met Asp Glu His Val Thr Lys Pro Leu Arg Arg Thr Asp Leu			
	1410	1415	1420
Val Ser Ala Ile Lys Arg Leu Val Thr Pro His Gly Ala His			
1425	1430	1435	

<210> 69

<211> 4317

<212> DNA

<213> Thanatephorus cucumeris

<220>

<221> CDS

<222> (1).. (4317)

<400> 69

atg gca ggt aca acg ggg gga cac ccg ttt acg gcg cac cta gtt gcg	48
Met Ala Gly Thr Thr Gly Gly His Pro Phe Thr Ala His Leu Val Ala	
1 5 10 15	
gtg ctg agt atc tat gag tta gga ccg gga cga cca gtg cgc gca ctg	96
Val Leu Ser Ile Tyr Glu Leu Gly Pro Gly Arg Pro Val Arg Ala Leu	
20 25 30	
ccg acc cgg agc tca cat tcc cat tcc tct tcc ggt tcc cgc cat gcg	144
Pro Thr Arg Ser Ser His Ser His Ser Ser Ser Gly Ser Arg His Ala	
35 40 45	
cgt gcg ctg tct gtg ccg ccg ttc cca cca ccg cca ccg atg tct ccg	192
Arg Ala Leu Ser Val Pro Pro Phe Pro Pro Pro Pro Pro Met Ser Pro	
50 55 60	
ccg aac gca ccg atc gac tac gta ggc gct gct ccg ctg ccc cga tac	240
Pro Asn Ala Pro Ile Asp Tyr Val Gly Ala Ala Pro Leu Pro Arg Tyr	
65 70 75 80	
gat gga ccg cgt gac tgg cag acg gat gcg gtc gag cga gca ctg ggc	288
Asp Gly Pro Arg Asp Trp Gln Thr Asp Ala Val Glu Arg Ala Leu Gly	
85 90 95	
cgt gtt gcc gcg cgg atg tac gcg gcc gag gcc cag ctg cag gac ctg	336
Arg Val Ala Ala Arg Met Tyr Ala Ala Glu Ala Gln Leu Gln Asp Leu	

100	105	110	
ctg agc cgc gag tcg agc aca tcc acc ccc gat ccc gct ctc tcg ccc			384
Leu Ser Arg Glu Ser Ser Thr Ser Thr Pro Asp Pro Ala Leu Ser Pro			
115	120	125	
cgc tcc aac ggc ctc aaa aaa cgc aga gag aac ccg gga aca ccc gat			432
Arg Ser Asn Gly Leu Lys Lys Arg Arg Glu Asn Pro Gly Thr Pro Asp			
130	135	140	
gag cgc gat ccg tgg cag act gtg cgc ttt caa gag gtc ggt gac cag			480
Glu Arg Asp Pro Trp Gln Thr Val Arg Phe Gln Glu Val Gly Asp Gln			
145	150	155	160
gac atg gat ccc gag cca gac acc cct gtt gcc cgc ccc aag gac aag			528
Asp Met Asp Pro Glu Pro Asp Thr Pro Val Ala Arg Pro Lys Asp Lys			
165	170	175	
gtc aag cct ggt acc att gac ctg agt aca ctc tcc cag ccc act ccg			576
Val Lys Pro Gly Thr Ile Asp Leu Ser Thr Leu Ser Gln Pro Thr Pro			
180	185	190	
ctc tcc aag gtg gcc acg gac aat ccg gtg ctg ccc aag cct ggt ccc			624
Leu Ser Lys Val Ala Thr Asp Asn Pro Val Leu Pro Lys Pro Gly Pro			
195	200	205	

cgc agc gca ccc acc agc agc gtc gga tcc atc atg cct ccc ttc acg	672
Arg Ser Ala Pro Thr Ser Ser Val Gly Ser Ile Met Pro Pro Phe Thr	
210 215 220	
tgc cac tcg tgc gga cgc ccc atg cag ggc ccc gct gcc ccc gat gtc	720
Cys His Ser Cys Gly Arg Pro Met Gln Gly Pro Ala Ala Pro Asp Val	
225 230 235 240	
ata cac gca ccc ggt ccc ctc gac gtt gtc acc cct gca ctt ggc atg	768
Ile His Ala Pro Gly Pro Leu Asp Val Val Thr Pro Ala Leu Gly Met	
245 250 255	
ggc ctc ggt ctc tct gac cat ggc gct gcc gag ctc aga cag aaa ctt	816
Gly Leu Gly Leu Ser Asp His Gly Ala Ala Glu Leu Arg Gln Lys Leu	
260 265 270	
ggc ttt ggc gat cac gaa gac gac acc ggt agt ccc ctt gtt ctc ccc	864
Gly Phe Gly Asp His Glu Asp Asp Thr Gly Ser Pro Leu Val Leu Pro	
275 280 285	
cct ggc cct ctc agt gct gct gcc ttt gag agc gct cca ggc atg tcc	912
Pro Gly Pro Leu Ser Ala Ala Ala Phe Glu Ser Ala Pro Gly Met Ser	
290 295 300	
gcc gtc gaa gaa ctc aag ctg ctc aag gcc cag gtc cag gat gtc gct	960
Ala Val Glu Glu Leu Lys Leu Leu Lys Ala Gln Val Gln Asp Val Ala	

305	310	315	320	
cgt gta tgc aag gcc gtc gcc gag ggt gat ttg tct caa aag att acc				1008
Arg Val Cys Lys Ala Val Ala Glu Gly Asp Leu Ser Gln Lys Ile Thr				
	325	330	335	
gtc ccc gtt caa ggt ccc gtc atg gtc cag ctc aag gat gtc atc aac				1056
Val Pro Val Gln Gly Pro Val Met Val Gln Leu Lys Asp Val Ile Asn				
	340	345	350	
acc atg gtc gat aaa cta ggc agg ttt gcg cag gag gtc act cgt gtc				1104
Thr Met Val Asp Lys Leu Gly Arg Phe Ala Gln Glu Val Thr Arg Val				
	355	360	365	
tcg ctc gaa gtc gga act gaa ggc cgg ctc ggt ggt cag gcc att gtt				1152
Ser Leu Glu Val Gly Thr Glu Gly Arg Leu Gly Gly Gln Ala Ile Val				
	370	375	380	
cgc gat gtc cgc gga aca tgg agc gaa ctc aca acc gtc gtc aat cgt				1200
Arg Asp Val Arg Gly Thr Trp Ser Glu Leu Thr Thr Val Val Asn Arg				
	385	390	395	400
ctc gcc gct aat ctc aca agc cag gtc cgg gga atc gca gaa gtc acc				1248
Leu Ala Ala Asn Leu Thr Ser Gln Val Arg Gly Ile Ala Glu Val Thr				
	405	410	415	

aag gca gtc gcc aag ggc gat ctc tcc aaa caa atc ggc gtc gat gca 1296

Lys Ala Val Ala Lys Gly Asp Leu Ser Lys Gln Ile Gly Val Asp Ala

420

425

430

aaa ggt gaa ata ttg gaa ttg aag aat acg gtt aat acc atg gtc gtc 1344

Lys Gly Glu Ile Leu Glu Leu Lys Asn Thr Val Asn Thr Met Val Val

435

440

445

cgg ttg cgt atg ttt gca ggc gaa gtc acc cga gtc gcg ctc gat gtc 1392

Arg Leu Arg Met Phe Ala Gly Glu Val Thr Arg Val Ala Leu Asp Val

450

455

460

ggc agt cgt ggt att cta ggc ggt cag gct tat gtc ccg gat gtc gag 1440

Gly Ser Arg Gly Ile Leu Gly Gly Gln Ala Tyr Val Pro Asp Val Glu

465

470

475

480

ggt gtt tgg caa gag ttg acg gat aat gta aat cgc atg tgc tcc aat 1488

Gly Val Trp Gln Glu Leu Thr Asp Asn Val Asn Arg Met Cys Ser Asn

485

490

495

ttg acc aac caa gtc cgt tcg att gcg ctc gtt act acc gcc gtc gcc 1536

Leu Thr Asn Gln Val Arg Ser Ile Ala Leu Val Thr Thr Ala Val Ala

500

505

510

gag ggt gac ctc aca cgt aaa atc gaa att gaa gtc gag ggc gaa atg 1584

Glu Gly Asp Leu Thr Arg Lys Ile Glu Ile Glu Val Glu Gly Glu Met

515	520	525	
ttg acg ctc aag aat acg gta aac agc atg gtg gac cag ctt tcg acg			1632
Leu Thr Leu Lys Asn Thr Val Asn Ser Met Val Asp Gln Leu Ser Thr			
530	535	540	
ttt gcg agc gaa gtc acg cgg gtc gcg ctc gag gtt ggc tcg atg ggt			1680
Phe Ala Ser Glu Val Thr Arg Val Ala Leu Glu Val Gly Ser Met Gly			
545	550	555	560
ata ctc ggt ggt cag gcg cag gtc gag ggt gta aaa gga act tgg gcc			1728
Ile Leu Gly Gly Gln Ala Gln Val Glu Gly Val Lys Gly Thr Trp Ala			
565	570	575	
gac ttg acg agg aat gtg aat aat atg gcg tcc aat cta acc aat caa			1776
Asp Leu Thr Arg Asn Val Asn Asn Met Ala Ser Asn Leu Thr Asn Gln			
580	585	590	
gtc cgt tcg atc gcc aag gtc acg acg gcc gtc gcg cac ggt gac ctg			1824
Val Arg Ser Ile Ala Lys Val Thr Thr Ala Val Ala His Gly Asp Leu			
595	600	605	
cgg cag ttt gtc gaa gtc gat gtc cag gga gag atg ctc atg ttg aag			1872
Arg Gln Phe Val Glu Val Asp Val Gln Gly Glu Met Leu Met Leu Lys			
610	615	620	

aac acg gtg aat agc atg gtg gct cag ctc gat acg ctc gcg agc gag	1920
Asn Thr Val Asn Ser Met Val Ala Gln Leu Asp Thr Leu Ala Ser Glu	
625 630 635 640	
gtg tcg cgt gtc gcg ctc gag gtc ggt atc gag ggt cga ctc ggt gga	1968
Val Ser Arg Val Ala Leu Glu Val Gly Ile Glu Gly Arg Leu Gly Gly	
645 650 655	
cag gct gtg gtt cag ggt gtg gag ggt gtg tgg aag gtt tta acg gac	2016
Gln Ala Val Val Gln Gly Val Glu Gly Val Trp Lys Val Leu Thr Asp	
660 665 670	
aat gtc aac ttg atg gct ctg aat ctg acg acc caa gtg cgg tct att	2064
Asn Val Asn Leu Met Ala Leu Asn Leu Thr Thr Gln Val Arg Ser Ile	
675 680 685	
gcg gct gtg acg act gcc gtg gcg cgt ggt gac ctt agc aag aat atc	2112
Ala Ala Val Thr Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Asn Ile	
690 695 700	
gat gtc gat gtc aag ggc gag att ttg gat ttg aag att acg gtc aat	2160
Asp Val Asp Val Lys Gly Glu Ile Leu Asp Leu Lys Ile Thr Val Asn	
705 710 715 720	
cgc atg acg gat agt ttg cgg ata ttc gct gct gaa gtg act cgt gtc	2208
Arg Met Thr Asp Ser Leu Arg Ile Phe Ala Ala Glu Val Thr Arg Val	

725	730	735	
gcg cgc gag gtc ggt acg ctc gga cga ctc ggc gga cag gcg ttt gtt	2256		
Ala Arg Glu Val Gly Thr Leu Gly Arg Leu Gly Gly Gln Ala Phe Val			
740	745	750	
cct ggt gtg gct ggc gtg tgg aag gat ttg acg gat aat gtg aat gtt	2304		
Pro Gly Val Ala Gly Val Trp Lys Asp Leu Thr Asp Asn Val Asn Val			
755	760	765	
atg gct gcc aat ttg acg ttg caa gta cga gct att gcc cga gtc aca	2352		
Met Ala Ala Asn Leu Thr Leu Gln Val Arg Ala Ile Ala Arg Val Thr			
770	775	780	
acg gcc gtg tcg gtc gga gac ttg acg acc aag gtc gaa ggc atc gat	2400		
Thr Ala Val Ser Val Gly Asp Leu Thr Thr Lys Val Glu Gly Ile Asp			
785	790	795	800
gtc gcg ggt gaa atc ttg gat ctc gtc aac acg atc aac gga atg gtg	2448		
Val Ala Gly Glu Ile Leu Asp Leu Val Asn Thr Ile Asn Gly Met Val			
805	810	815	
gac cag ctc gcc gtg ttt gcg gcc gag gtc acg agg gtc gca cgc gaa	2496		
Asp Gln Leu Ala Val Phe Ala Ala Glu Val Thr Arg Val Ala Arg Glu			
820	825	830	

gtc gga acc gag ggt cgg ttg ggt gtt cag gct cgc gtc gaa ggt atg	2544
Val Gly Thr Glu Gly Arg Leu Gly Val Gln Ala Arg Val Glu Gly Met	
835 840 845	
caa ggc agc tgg cag gcg att acc gta tct gta aac acg atg gct gcc	2592
Gln Gly Ser Trp Gln Ala Ile Thr Val Ser Val Asn Thr Met Ala Ala	
850 855 860	
aac ttg acg tcc caa gtg cgt ggg ttt gcg caa atc tcg gca gcg gcg	2640
Asn Leu Thr Ser Gln Val Arg Gly Phe Ala Gln Ile Ser Ala Ala Ala	
865 870 875 880	
acc gac gga gac ttt acg cgc ttc atc acg gtc gaa gcg agc gga gag	2688
Thr Asp Gly Asp Phe Thr Arg Phe Ile Thr Val Glu Ala Ser Gly Glu	
885 890 895	
atg gac tcg ctc aag acg cag atc aat cag atg gtg tac aac ctc cgg	2736
Met Asp Ser Leu Lys Thr Gln Ile Asn Gln Met Val Tyr Asn Leu Arg	
900 905 910	
gag agt att cag agg aac acg gct gcg cgt gag gct gct gag ctt gcg	2784
Glu Ser Ile Gln Arg Asn Thr Ala Ala Arg Glu Ala Ala Glu Leu Ala	
915 920 925	
aat cgg tcc aag tcc gag ttc ctt gcc aac atg tcg cac gag att cga	2832
Asn Arg Ser Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Ile Arg	

930	935	940	
acg ccg atg aac ggg att att ggc atg acg gat ctc acg ctt gat acc			2880
Thr Pro Met Asn Gly Ile Ile Gly Met Thr Asp Leu Thr Leu Asp Thr			
945	950	955	960
gaa ctt aca cgg acg caa aaa gaa aac ttg ttg ctc gtt cac cag ctc			2928
Glu Leu Thr Arg Thr Gln Lys Glu Asn Leu Leu Leu Val His Gln Leu			
	965	970	975
gcc aag tct cta ttg ctt att atc gat gat att ctt gat att tcc aag			2976
Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu Asp Ile Ser Lys			
	980	985	990
atc gag gct ggc agg atg acc atg gaa caa gtc acg tat tct ctc cgc			3024
Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr Tyr Ser Leu Arg			
	995	1000	1005
ggc act gca ttc ggt atc ctc aag acc ctt gtc gtc cgg gct cac caa			3072
Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val Arg Ala His Gln			
1010	1015	1020	
caa aat ctc aac ctg ttc tac gaa gtc gat ccc gag att ccg gac caa			3120
Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu Ile Pro Asp Gln			
1025	1030	1035	1040

gtc att ggc gat tcg ctc cgt ctg cga caa gtc att acc aac ctc gtc 3168

Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile Thr Asn Leu Val

1045

1050

1055

gga aac gct atc aag ttc act ccc agc aag ccc aac aaa aag ggc atg 3216

Gly Asn Ala Ile Lys Phe Thr Pro Ser Lys Pro Asn Lys Lys Gly Met

1060

1065

1070

gtc tgc ctc tcg tgc aag ctc atc tcg atg gac gag cag aat gtg acg 3264

Val Cys Leu Ser Cys Lys Leu Ile Ser Met Asp Glu Gln Asn Val Thr

1075

1080

1085

gtt cgg ttc tgt gtc gag gac acg ggt atc ggt atc aag cag gat aaa 3312

Val Arg Phe Cys Val Glu Asp Thr Gly Ile Gly Ile Lys Gln Asp Lys

1090

1095

1100

ctc gcg atc atc ttt gat acg ttc tgt caa gcc gat ggg tcc acg act 3360

Leu Ala Ile Ile Phe Asp Thr Phe Cys Gln Ala Asp Gly Ser Thr Thr

1105

1110

1115

1120

cgt gaa tac ggt ggt acc ggt ctc ggc ttg tcc atc tcg aaa cga ctc 3408

Arg Glu Tyr Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg Leu

1125

1130

1135

gtg tct ctg atg aat ggc caa atg tgg gtc gag tcc gag gtc gga gtc 3456

Val Ser Leu Met Asn Gly Gln Met Trp Val Glu Ser Glu Val Gly Val

1140	1145	1150	
ggg tcc cgc ttc tac ttt acg atc acc gcc gaa atc tcc cgg ccg aac			3504
Gly Ser Arg Phe Tyr Phe Thr Ile Thr Ala Glu Ile Ser Arg Pro Asn			
1155	1160	1165	
atg gcg caa agt ctg caa aag gtc gcg atc tac aag gag cgc acg atc			3552
Met Ala Gln Ser Leu Gln Lys Val Ala Ile Tyr Lys Glu Arg Thr Ile			
1170	1175	1180	
ttg ttt gtc gat act ctg ggc gac cgg tcg ggt gtg gcg gag cgt atc			3600
Leu Phe Val Asp Thr Leu Gly Asp Arg Ser Gly Val Ala Glu Arg Ile			
1185	1190	1195	1200
gaa gag ctg cag ctg cgt ccg ttt gtc gtg cgg gat atc agc cag gtg			3648
Glu Glu Leu Gln Leu Arg Pro Phe Val Val Arg Asp Ile Ser Gln Val			
1205	1210	1215	
gcg gac aag gcc aag att ccg ttt atc gat acg gtg att gtg gat tcg			3696
Ala Asp Lys Ala Lys Ile Pro Phe Ile Asp Thr Val Ile Val Asp Ser			
1220	1225	1230	
ctc gag gtg act gag aaa ttg cgc gag ttg gat cat ttg agg tat acc			3744
Leu Glu Val Thr Glu Lys Leu Arg Glu Leu Asp His Leu Arg Tyr Thr			
1235	1240	1245	

ccg gcc gtg ctc ttg acg cca gtt atg ccc cga ctg aat ctg acg tgg 3792

Pro Ala Val Leu Leu Thr Pro Val Met Pro Arg Leu Asn Leu Thr Trp

1250

1255

1260

tgt ctt gag aac ttt atc tcg ggt cat gtc gcg acc ccg tct tcg ctc 3840

Cys Leu Glu Asn Phe Ile Ser Gly His Val Ala Thr Pro Ser Ser Leu

1265

1270

1275

1280

gac gat ctt gcc gag gcg ctc gca aag gga ctg gaa gcc aac gca tct 3888

Asp Asp Leu Ala Glu Ala Leu Ala Lys Gly Leu Glu Ala Asn Ala Ser

1285

1290

1295

cag ccc gag gtt acg ccc agc gac gtt gcg tac gac att cta ctg gcc 3936

Gln Pro Glu Val Thr Pro Ser Asp Val Ala Tyr Asp Ile Leu Leu Ala

1300

1305

1310

gaa gac aat gtt gtc aac caa cgt gtg gcc gtc aag att ctc gaa aag 3984

Glu Asp Asn Val Val Asn Gln Arg Val Ala Val Lys Ile Leu Glu Lys

1315

1320

1325

ttt ggt cac acg gtt cag att gcc gag aat gga cag ttt gcg gtc gac 4032

Phe Gly His Thr Val Gln Ile Ala Glu Asn Gly Gln Phe Ala Val Asp

1330

1335

1340

gct gtc aag gct cga tac gaa caa gag aag atg ttt gat gtc att ctt 4080

Ala Val Lys Ala Arg Tyr Glu Gln Glu Lys Met Phe Asp Val Ile Leu

1345	1350	1355	1360	
atg gac gtg tct atg ccg ttc atg ggt gga atg gag gca aca gaa att				4128
Met Asp Val Ser Met Pro Phe Met Gly Gly Met Glu Ala Thr Glu Ile				
	1365	1370	1375	
att cgc gcg ttt gag aag gaa aag ggc atc cgc cgc acg cct att atc				4176
Ile Arg Ala Phe Glu Lys Glu Lys Gly Ile Arg Arg Thr Pro Ile Ile				
	1380	1385	1390	
gct ctc aca gcg cac gcg atg att ggt gat cgt gag cgc tgt atc cag				4224
Ala Leu Thr Ala His Ala Met Ile Gly Asp Arg Glu Arg Cys Ile Gln				
	1395	1400	1405	
gct ggc atg gat gaa cac gtt acg aaa ccg ttg agg aga acc gat ctc				4272
Ala Gly Met Asp Glu His Val Thr Lys Pro Leu Arg Arg Thr Asp Leu				
	1410	1415	1420	
gtg agc gcg atc aaa cgc ctc gta aca ccc cac ggt gcc cac taa				4317
Val Ser Ala Ile Lys Arg Leu Val Thr Pro His Gly Ala His				
1425	1430	1435		

<210> 70

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 70

cgaagtcgat cccgagattc cggacc

26

<210> 71

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 71

cccgactccg acctcggact cgacccac

28

<210> 72

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 72

ggtgagcccg gacgacaagg gtcttgag

28

<210> 73

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed.
oligonucleotide primer for PCR

<400> 73

attcgctcga ggtgactgag aa

22

<210> 74

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 74

ttacctcatc gctatctctt

20

<210> 75

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 75

aaggtcgcga tctacaagga gc

22

<210> 76

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 76

atggacgtgt ctatgccgtt ca

22

<210> 77

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 77

cttcgaccgt gatgaagcgc gta

23

<210> 78

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 78

acgaagacga caccggtagt cc

22

<210> 79

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 79

atcgcagaag tcaccaaggc agt

23

<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 80

gccaccgatg tctccgccga ac

22

<210> 81

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 81

cttgctaagg tcaccacgcg cca

23

<210> 82

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 82

ttctaggtgg tcaggcttat gtcc

24

<210> 83

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 83

ccagctgcag gacctgctga gc

22

<210> 84

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 84

ctcaagaccc ttgtcgtccg ggctcacc

28

<210> 85

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 85

ggaactagta tggcaggtac aacgggggga cacc

34

<210> 86

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 86

tgcaagcttt tagtgggcac cgtggggtgt tacg

34

<210> 87

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 87

tttctgcaca atatttcaag ctatacc

27

<210> 88

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for PCR

<400> 88

gacctagact tcaggttgtc taactcc

27

<210> 89

<211> 372

<212> DNA

<213> Phytophthora infestans

<220>

<221> CDS

<222> (1).. (372)

<400> 89

cac gag att cgc aca ccc atg aat ggg att att ggc atg acg gat ctc 48

His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Asp Leu

1

5

10

15

acg ctt gat acc gaa ctt aca cgg acg caa aaa gaa aac ttg ttg ctc 96

Thr Leu Asp Thr Glu Leu Thr Arg Thr Gln Lys Glu Asn Leu Leu Leu

20	25	30	
gtt cac cag ctc gcc aag tct cta ttg ctc att atc gat gat att ctt			144
Val His Gln Leu Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu			
35	40	45	
gat att tcc aag atc gag gct ggc agg atg acc atg gaa caa gtc acg			192
Asp Ile Ser Lys Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr			
50	55	60	
tat tct ctc cgc ggc acc gca ttc ggt atc ctc aag acc ctt gtc gtc			240
Tyr Ser Leu Arg Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val			
65	70	75	80
cgg gct cac caa caa aat ctc aac ctg ttc tac gaa gtc gat ccc gag			288
Arg Ala His Gln Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu			
85	90	95	
att ccg gac caa gtc att ggt gat tcg ctc cgt ctg cga caa gtc att			336
Ile Pro Asp Gln Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile			
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Thr Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu			
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<213> *Phytophthora infestans*

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Val His Gln Leu Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu

35 40 45

Asp Ile Ser Lys Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr

50 55 60

Tyr Ser Leu Arg Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val

65 70 75 80

Arg Ala His Gln Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu

85 90 95

Ile Pro Asp Gln Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile

100 105 110

Thr Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu

115 120